

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2004, 15:54:37 ; Search time 43.05 Seconds
(without alignments)
4069.212 Million cell updates/sec

Title: US-10-054-680-4
Perfect score: 3228
Sequence: 1 MAWLRLQPLTSAFLHFGGLVT.....ADYGRRGGQEDSRDGKASIG 620

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Query				Description
Result No.	Score	Match	Length	DB	ID	
1	3228	100.0	620	5	ABB81914	Abb81914 Human ion
2	3093	95.8	595	6	ABR40134	Abr40134 Human 690
3	3093	95.8	921	5	ABP74104	Abp74104 Human TRI
4	3093	95.8	921	5	ABB83246	Abb83246 Human tra
5	3093	95.8	921	5	ABB81913	Abb81913 Human ion
6	3093	95.8	921	5	ABB81915	Abb81915 Human ion
7	3093	95.8	922	5	ABB81916	Abb81916 Human ion
8	3093	95.8	922	5	ABB81917	Abb81917 Human ion
9	3093	95.8	925	6	ABU12042	Abu12042 Human NOV

10	3093	95.8	927	5	AAM47745	Aam47745	Human nat
11	3093	95.8	928	6	ABU12041	Abu12041	Human NOV
12	3016	93.4	927	5	ABB83247	Abb83247	Human tra
13	2940	91.1	895	6	ABU12043	Abu12043	Human NOV
14	2147.5	66.5	970	5	AAE18291	Aae18291	Bovine NC
15	2143.5	66.4	609	4	AAM13701	Aam13701	Peptide #
16	2143.5	66.4	609	4	ABB32633	Abb32633	Peptide #
17	2143.5	66.4	609	4	AAM26102	Aam26102	Peptide #
18	2143.5	66.4	609	4	ABB18131	Abb18131	Protein #
19	2143.5	66.4	609	4	AAM53461	Aam53461	Human bra
20	2143.5	66.4	609	4	ABG47486	Abg47486	Human liv
21	2143.5	66.4	609	5	ABG35474	Abg35474	Human pep
22	1961	60.7	921	7	AAO27170	Aao27170	Human 465
23	1961	60.7	952	3	AAB41497	Aab41497	Human ORF
24	1339.5	41.5	950	4	ABB61721	Abb61721	Drosophil
25	362.5	11.2	539	3	AAY58044	Aay58044	Arabidops
26	203.5	6.3	106	6	ABR40136	Abr40136	69039 pro
27	203.5	6.3	618	4	AAM78712	Aam78712	Human pro
28	203.5	6.3	661	5	ABB84485	Abb84485	Human NCK
29	203.5	6.3	661	6	AAO29752	Aao29752	Human 577
30	203.5	6.3	661	7	ADE54756	Ade54756	Human Pro
31	202	6.3	6304	6	ABU09236	Abu09236	Human neu
32	201.5	6.2	670	7	ADE54754	Ade54754	Rat Prote
33	197	6.1	546	4	ABB12262	Abb12262	Human ver
34	186.5	5.8	644	7	ADE31661	Ade31661	Human 692
35	184	5.7	2092	6	ABU09234	Abu09234	Rat neuro
36	180.5	5.6	603	5	AAE22088	Aae22088	Human nov
37	172.5	5.3	630	5	ABP69673	Abp69673	Human pol
38	171.5	5.3	2071	4	AAE10949	Aae10949	Mouse mas
39	171.5	5.3	2780	4	AAE10924	Aae10924	Mouse mon
40	162.5	5.0	856	4	ABB60425	Abb60425	Drosophil
41	161	5.0	759	5	ABG61545	Abg61545	Human tra
42	161	5.0	2701	5	ABP74125	Abp74125	Human TRI
43	161	5.0	2753	6	ADA05806	Ada05806	Human NOV
44	161	5.0	2753	6	ADA05800	Ada05800	Human NOV
45	161	5.0	3838	6	ADA05802	Ada05802	Human NOV

ALIGNMENTS

RESULT 1

ABB81914

ID ABB81914 standard; protein; 620 AA.

XX

AC ABB81914;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #2.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral.

XX

OS Homo sapiens.

XX

PN WO200259316-A2.

XX PD 01-AUG-2002.
XX
PF 22-JAN-2002; 2002WO-US001817.
XX
PR 23-JAN-2001; 2001US-0263384P.
XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Friddle CJ, Hilbun E;
XX
DR WPI; 2002-599791/64.
DR N-PSDB; ABQ78862.
XX
PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.
XX
PS Claim 4; Page 40-41; 42pp; English.
XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a NHIEP of the invention
XX
SQ Sequence 620 AA;

Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQDLVEMANYYALSHQQKSRIFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQDLVEMANYYALSHQQKSRIFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVCDRQE	600
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVCDRQE	600
Qy	601	ADYGRRGGQEDSRDGKASIG	620
Db	601	ADYGRRGGQEDSRDGKASIG	620

RESULT 2

ABR40134

ID ABR40134 standard; protein; 595 AA.

XX

AC ABR40134;

XX

DT 04-JUL-2003 (first entry)

XX

DE Human 69039 protein.

XX

KW Human; 69039; neuroprotective; gene therapy; haematopoietic disorder;

KW Na⁺/Ca²⁺ exchanger; ion transporter; neural tissue;

KW neurological disorder.

XX

OS Homo sapiens.

XX

PN WO2003029410-A2.

XX

PD 10-APR-2003.

XX

PF 27-SEP-2002; 2002WO-US030817.

XX

PR 28-SEP-2001; 2001US-0325737P.

XX

PA (MILL-) MILLENIUM PHARM INC.

XX

PI Carroll JM;

XX

DR WPI; 2003-381617/36.

DR N-PSDB; ACC00414.

XX

PT Identifying a nucleic acid molecule associated with a disorder for

PT preparing a composition for treating hematopoietic or neurological
PT disorder by detecting the presence of a nucleic acid molecule in the
PT sample that is amplified.

XX

PS Example 1; Page 110; 133pp; English.

XX

CC The present sequence is the protein sequence for human 69039, a novel
CC Na⁺/Ca²⁺ exchanger family member (ion transporter). 69039 was shown to be
CC expressed in human haematopoietic cells, e.g. CD34-expressing progenitor
CC cells as well as in neural tissues, e.g. brain cortex and hypothalamus.
CC 69039 may therefore be used for preparing a composition for treating
CC haematopoietic or neurological disorder

XX

SQ Sequence 595 AA;

Query Match 95.8%; Score 3093; DB 6; Length 595;

Best Local Similarity 100.0%; Pred. No. 5.5e-308;

Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRIFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRIFYRIQATR	360
Qy	361	MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRITSGARGTVIVPFRITVEGTAKGGGEDFEDTYGELEFKNDET	595

RESULT 3

ABP74104

ID ABP74104 standard; protein; 921 AA.
 XX
 AC ABP74104;
 XX
 DT 30-JAN-2003 (first entry)
 XX
 DE Human TRICH SEQ ID NO 9.
 XX
 KW Human; TRICH; transporter and ion channel; transport disorder;
 KW cystic fibrosis; diabetes mellitus; Parkinson's disease; cancer;
 KW neurological disorder; Alzheimer's disease; Huntington's disease;
 KW immunological disorder; AIDS; asthma; cell proliferative disorder;
 KW transgenic; gene therapy; neuroprotective; antidiabetic; cytostatic;
 KW antiparkinsonian; hypotensive; nootropic; antianaemic; anticonvulsant;
 KW cerebroprotective; cardiast; anti-HIV; human immunodeficiency virus;
 KW antiasthmatic; antiatherosclerotic; antigout; antiarteriosclerotic;
 KW hepatotropic; antiinflammatory; virucide; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200246415-A2.
 XX
 PD 13-JUN-2002.
 XX
 PF 05-DEC-2001; 2001WO-US046963.
 XX
 PR 08-DEC-2000; 2000US-0254303P.
 PR 15-DEC-2000; 2000US-0256190P.
 PR 21-DEC-2000; 2000US-0257504P.
 PR 12-JAN-2001; 2001US-0261546P.
 PR 19-JAN-2001; 2001US-0262832P.
 PR 26-JAN-2001; 2001US-0264377P.
 PR 02-FEB-2001; 2001US-0266019P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Lee EA, Baughn MR, Yue H, Ding L, Raumann BE, Hafalia AJA;
 PI Khan FA, Nguyen DB, Elliott VS, Ramkumar J, Walia NK, Ison CH;
 PI Lu Y, Gandhi AR, Warren BA, Duggan BM, Tribouley CM, Burford N;
 PI Lu DAM, Lal PG, Yao MG, Xu Y, Bruns CM, Thangavelu K, Swarnakar A;
 PI Tang YT, Azimzai Y, Thornton M, Arvizu C, Policky JL;
 XX
 DR WPI; 2002-519667/55.
 DR N-PSDB; ABZ33735.
 XX
 PT Novel human transporter and ion channel polypeptide, useful in diagnosis,
 PT prevention or treatment of transport, neurological, muscle, immunological
 PT and cell proliferative disorders.
 XX
 PS Claim 64; SEQ ID NO 9; 146pp + Sequence Listing; English.
 XX
 CC The invention relates to human transporter and ion channel polypeptide

CC (TRICH) (I) selected from one of 32 polypeptide sequences (ABP74096-
 CC ABP74127), a naturally occurring polypeptide comprising a sequence having
 CC at least sequence 90 % identity to (I) or a biologically active or
 CC immunogenic fragment of (I). (I) is useful for screening a compound for
 CC effectiveness as an agonist or antagonist, for screening a compound that
 CC specifically binds (I) or modulates the activity of (I) and for preparing
 CC a polyclonal or monoclonal antibody by hybridoma technology.
 CC Polynucleotides (II, ABZ33727-ABZ33758) encoding (I) are useful for
 CC screening a compound altering gene expression. (I) and (II) are useful in
 CC a diagnostic tests for a condition or a disease associated with the
 CC expression of TRICH in a biological sample, especially disorders selected
 CC from a transport disorder such as cystic fibrosis, diabetes mellitus,
 CC Parkinson's disease, cardiac disorders, neurological disorders such as
 CC Alzheimer's disease, Huntington's disease, muscle disorders,
 CC immunological disorder such as AIDS, asthma and atherosclerosis, and cell
 CC proliferative disorder such as arteriosclerosis, cirrhosis, hepatitis and
 CC cancer. (II) is useful for creating knock-in humanised animals or
 CC transgenic animals to model human diseases, in somatic or germline gene
 CC therapy, to generate a transcript image of a tissue or cell type, for
 CC detecting differences in the chromosomal location due to translocation,
 CC inversion among normal, carrier or affected individuals and for mapping
 CC genomic sequences. Note: The sequence data for this patent is not
 CC represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 921 AA;

Query Match 95.8%; Score 3093; DB 5; Length 921;
 Best Local Similarity 100.0%; Pred. No. 1.1e-307;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420

Db 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
 Qy 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF 480
 Qy 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 Qy 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

RESULT 4

ABB83246

ID ABB83246 standard; protein; 921 AA.

XX

AC ABB83246;

XX

DT 21-AUG-2002 (first entry)

XX

DE Human transporter protein.

XX

KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;
 KW spleen; testis; leukocyte; foetal brain; chromosome 14.

XX

OS Homo sapiens.

XX

PN WO200233086-A2.

XX

PD 25-APR-2002.

XX

PF 17-OCT-2001; 2001WO-US032152.

XX

PR 17-OCT-2000; 2000US-0240836P.

PR 13-MAR-2001; 2001US-00804474.

XX

PA (PEKE) PE CORP NY.

XX

PI Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;

PI Beasley EM;

XX

DR WPI; 2002-479677/51.

DR N-PSDB; ABN83428, ABN83429.

XX

PT Human transporter peptide related to sodium/calcium exchanger subfamily
 PT for identifying modulators useful for treating a disease or condition
 PT mediated by human transporter protein.

XX

PS Claim 1; Fig 2; 200pp; English.

XX

CC The present sequence is a human transporter protein, which is related to
 CC the sodium/calcium exchanger subfamily. Experimental data indicates
 CC expression of the transporter gene in humans in brain, heart, kidney,
 CC lung, spleen, testis, leukocyte and foetal brain. The gene of the

CC transporter was mapped to chromosome 14 by ePCR
XX
SQ Sequence 921 AA;

Query Match 95.8%; Score 3093; DB 5; Length 921;
Best Local Similarity 100.0%; Pred. No. 1.1e-307;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAAFNMF 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAAFNMF 180

Qy    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHHKRYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 FPVCVLLAWVADKRLLFYKYMHHKRYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR 360

Qy    361 MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy    541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
```

RESULT 5
ABB81913
ID ABB81913 standard; protein; 921 AA.
XX
AC ABB81913;
XX
DT 09-OCT-2002 (first entry)
XX

DE Human ion exchanger protein #1.
 XX
 KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral.
 XX
 OS Homo sapiens.
 XX
 PN WO200259316-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001817.
 XX
 PR 23-JAN-2001; 2001US-0263384P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Friddle CJ, Hilbun E;
 XX
 DR WPI; 2002-599791/64.
 DR N-PSDB; ABQ78861.
 XX
 PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.
 XX
 PS Claim 2; Page 37-39; 42pp; English.
 XX
 CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence represents a NHIEP of the invention
 XX
 SQ Sequence 921 AA;

Query Match 95.8%; Score 3093; DB 5; Length 921;
 Best Local Similarity 100.0%; Pred. No. 1.le-307;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180

Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 6

ABB81915

ID ABB81915 standard; protein; 921 AA.

XX

AC ABB81915;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 Asp/Gly mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
 KW mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 630

FT /note= "Wild-type Asp substituted by Gly"

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX
PA (LEXI-) LEXICON GENETICS INC.
XX
PI Friddle CJ, Hilbun E;
XX
DR WPI; 2002-599791/64.
XX
PT Novel polynucleotides encoding human ion exchanger proteins that are
PT structurally related to mammalian sodium-calcium exchanger proteins,
PT useful for drug screening, diagnosis and in gene therapy of biological
PT disorders.
XX
PS Disclosure; Page; 42pp; English.
XX
CC The invention relates to a novel human ion exchanger protein (NHIEP),
CC that shares structural similarity with mammalian sodium-calcium exchanger
CC proteins, and potassium dependent versions of the same. The NHIEP of the
CC invention has nootropic, cytostatic, antiarthritic, and virucide
CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
CC or to therapeutically augment the efficacy of chemotherapeutic agents
CC used in the treatment of cancer, arthritis, or as antiviral agents. The
CC sequence represents a mutant form of a NHIEP of the invention. Note: The
CC present sequence is not shown in the specification but is derived from
CC the human NHIEP sequence shown as SEQ ID 2 (ABB81913)
XX
SQ Sequence 921 AA;

Query Match 95.8%; Score 3093; DB 5; Length 921;
Best Local Similarity 100.0%; Pred. No. 1.1e-307;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRKHHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRKHHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420

Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 7

ABB81916

ID ABB81916 standard; protein; 922 AA.
 XX
 AC ABB81916;
 XX
 DT 09-OCT-2002 (first entry)
 XX
 DE Human ion exchanger protein #1 Ala mutant.
 XX
 KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
 KW mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 704. .705
 FT /note= "Wild-type Ala Ala substituted by Ala Ala Ala"
 XX
 PN WO200259316-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 22-JAN-2002; 2002WO-US001817.
 XX
 PR 23-JAN-2001; 2001US-0263384P.
 XX
 PA (LEXI-) LEXICON GENETICS INC.
 XX
 PI Friddle CJ, Hilbun E;
 XX
 DR WPI; 2002-599791/64.
 XX
 PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.
 XX
 PS Disclosure; Page; 42pp; English.

XX
 CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence represents a mutant form of a NHIEP of the invention. Note: The
 CC present sequence is not shown in the specification but is derived from
 CC the human NHIEP sequence shown as SEQ ID 2 (ABB81913)
 XX
 SQ Sequence 922 AA;

Query Match 95.8%; Score 3093; DB 5; Length 922;
 Best Local Similarity 100.0%; Pred. No. 1.2e-307;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKDIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKDIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRFYRIQATR	360
Qy	361	MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRITSGARGTVIVFPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 8

ABB81917

ID ABB81917 standard; protein; 922 AA.

XX

AC ABB81917;

XX

DT 09-OCT-2002 (first entry)

XX

DE Human ion exchanger protein #1 Asp/Gly+Ala mutant.

XX

KW Human; ion exchanger protein; NHIEP; nootropic; cytostatic; gene therapy;
 KW antiarthritic; virucide; chemotherapeutic; cancer; arthritis; antiviral;
 KW mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 630

FT /note= "Wild-type Asp substituted by Gly"

FT Misc-difference 704. .705

FT /note= "Wild-type Ala Ala substituted by Ala Ala Ala"

XX

PN WO200259316-A2.

XX

PD 01-AUG-2002.

XX

PF 22-JAN-2002; 2002WO-US001817.

XX

PR 23-JAN-2001; 2001US-0263384P.

XX

PA (LEXI-) LEXICON GENETICS INC.

XX

PI Friddle CJ, Hilbun E;

XX

DR WPI; 2002-599791/64.

XX

PT Novel polynucleotides encoding human ion exchanger proteins that are
 PT structurally related to mammalian sodium-calcium exchanger proteins,
 PT useful for drug screening, diagnosis and in gene therapy of biological
 PT disorders.

XX

PS Disclosure; Page; 42pp; English.

XX

CC The invention relates to a novel human ion exchanger protein (NHIEP),
 CC that shares structural similarity with mammalian sodium-calcium exchanger
 CC proteins, and potassium dependent versions of the same. The NHIEP of the
 CC invention has nootropic, cytostatic, antiarthritic, and virucide
 CC activity. The polynucleotide may have a use in gene therapy. NHIEPs can
 CC be targeted by drugs, oligos, antibodies etc., in order to treat disease
 CC or to therapeutically augment the efficacy of chemotherapeutic agents
 CC used in the treatment of cancer, arthritis, or as antiviral agents. The
 CC sequence represents a mutant form of a NHIEP of the invention. Note: The
 CC present sequence is not shown in the specification but is derived from

CC the human NHIEP sequence shown as SEQ ID 2 (ABB81913)
XX
SQ Sequence 922 AA;

Query Match 95.8%; Score 3093; DB 5; Length 922;
Best Local Similarity 100.0%; Pred. No. 1.2e-307;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180

Qy    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHHKRYRDKHKGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 FPVCVLLAWVADKRLLFYKYMHHKRYRDKHKGIIETEGDHPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRIFYRIQATR 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRIFYRIQATR 360

Qy    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy    541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
```

RESULT 9
ABU12042
ID ABU12042 standard; protein; 925 AA.
XX
AC ABU12042;
XX
DT 19-FEB-2003 (first entry)
XX

DE Human NOV1b CG56558-02 protein SEQ ID 4.
 XX
 KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200281625-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010366.
 XX
 PR 03-APR-2001; 2001US-0281086P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 06-APR-2001; 2001US-0282020P.
 PR 10-APR-2001; 2001US-0282930P.
 PR 12-APR-2001; 2001US-0283444P.
 PR 12-APR-2001; 2001US-0283512P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285381P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 25-APR-2001; 2001US-0286292P.
 PR 07-JUN-2001; 2001US-0296692P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 08-AUG-2001; 2001US-0311003P.
 PR 13-AUG-2001; 2001US-0311973P.
 PR 16-AUG-2001; 2001US-0312901P.
 PR 14-SEP-2001; 2001US-0322283P.
 PR 05-OCT-2001; 2001US-0327448P.
 PR 31-DEC-2001; 2001US-0345734P.
 PR 03-JAN-2002; 2002US-0345755P.
 PR 04-FEB-2002; 2002US-0354391P.
 PR 02-APR-2002; 2002US-00114153.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
 PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
 PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
 PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
 PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
 PI Mazur A;
 XX
 DR WPI; 2003-046862/04.
 DR N-PSDB; ABX56262.
 XX
 PT New isolated NOVX polypeptide useful for treating cardiomyopathy,

PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.

XX

PS Claim 1; Page 85; 425pp; English.

XX

CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments
CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306

XX

SQ Sequence 925 AA;

Query Match 95.8%; Score 3093; DB 6; Length 925;

Best Local Similarity 100.0%; Pred. No. 1.2e-307;

Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQQKSRAFYRIQATR	360

Qy 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

RESULT 10

AAM47745

ID AAM47745 standard; protein; 927 AA.

XX

AC AAM47745;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human natrium(+)-calcium(2+) exchanger form 3 protein, HNCX3.

XX

KW Human; Natrium(+)-Calcium(2+) exchanger form 3; HNCX3; chromosome 14;
 KW cardiac failure; myocardial infarction; cardiac hypertrophy; arrhythmia;
 KW myocarditis; pulmonary hypertension; cardiotoxicity; cardiant; Vaccine;
 KW coronary heart disease; renal failure; ischaemic disorder;
 KW Antiarrhythmic; Vasotropic; Hypotensive; cardiovascular disorder.

XX

OS Homo sapiens.

XX

PN WO200183744-A2.

XX

PD 08-NOV-2001.

XX

PF 30-APR-2001; 2001WO-EP004886.

XX

PR 02-MAY-2000; 2000EP-00109080.

XX

PA (MERE) MERCK PATENT GMBH.

XX

PI Wilm C;

XX

DR WPI; 2002-041493/05.

DR

N-PSDB; ABA04756.

XX

PT New polypeptide, useful as vaccines for inducing immune response against
 PT diseases such as myocardial infarction, arrhythmia, ischemic disorders,
 PT renal disorders in mammal.

XX

PS Claim 1; Page 38-41; 41pp; English.

XX

CC The present sequence is the protein sequence for human Natrium(+)-Calcium

CC (2+) exchanger form 3 (HNCX3). The HNCX3 gene maps to human chromosome
 CC 14. HNCX3 and its coding sequence are useful for treating acute and
 CC chronic cardiac failure of different aetiologies, myocardial infarction,
 CC cardiac hypertrophy, arrhythmia, myocarditis, pulmonary hypertension,
 CC cardiotoxicity (e.g. induced by chemotherapy), coronary heart disease,
 CC acute and chronic renal failure, ischaemic disorders of skeletal muscle
 CC and ischaemic brain disorders of different aetiologies

XX

SQ Sequence 927 AA;

Query Match 95.8%; Score 3093; DB 5; Length 927;
 Best Local Similarity 100.0%; Pred. No. 1.2e-307;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNIIKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGDMSTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGDMSTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 11
 ABU12041

ID ABU12041 standard; protein; 928 AA.
 XX
 AC ABU12041;
 XX
 DT 19-FEB-2003 (first entry)
 XX
 DE Human NOV1a CG56258-01 protein SEQ ID 2.
 XX
 KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;
 KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;
 KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;
 KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;
 KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;
 KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;
 KW metabolic syndrome X; wasting disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200281625-A2.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WO-US010366.
 XX
 PR 03-APR-2001; 2001US-0281086P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 06-APR-2001; 2001US-0282020P.
 PR 10-APR-2001; 2001US-0282930P.
 PR 12-APR-2001; 2001US-0283444P.
 PR 12-APR-2001; 2001US-0283512P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285381P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 25-APR-2001; 2001US-0286292P.
 PR 07-JUN-2001; 2001US-0296692P.
 PR 26-JUN-2001; 2001US-0300883P.
 PR 08-AUG-2001; 2001US-0311003P.
 PR 13-AUG-2001; 2001US-0311973P.
 PR 16-AUG-2001; 2001US-0312901P.
 PR 14-SEP-2001; 2001US-0322283P.
 PR 05-OCT-2001; 2001US-0327448P.
 PR 31-DEC-2001; 2001US-0345734P.
 PR 03-JAN-2002; 2002US-0345755P.
 PR 04-FEB-2002; 2002US-0354391P.
 PR 02-APR-2002; 2002US-00114153.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Padigaru M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;
 PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;
 PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
 PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
 PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;

PI Mazur A;
 XX
 DR WPI; 2003-046862/04.
 DR N-PSDB; ABX56261.
 XX
 PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
 PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
 PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
 PT cancer.
 XX
 PS Claim 1; Page 84; 425pp; English.
 XX
 CC This invention describes novel polypeptides, termed NOVX which have
 CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
 CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
 CC cardiant and immunomodulatory activity. The polypeptide and any
 CC antibodies generated from it are useful in the manufacture of a
 CC medicament for treating a syndrome associated with a human disease
 CC selected from a pathology associated with the NOVX polypeptide. Fragments
 CC and portions of the polynucleotides encoding NOVX polypeptides are useful
 CC to map the location of NOVX genes on a chromosome, to identify
 CC individuals from minute biological samples, as DNA markers for
 CC restriction fragment length polymorphism (RFLP), and are useful to
 CC prepare polymerase chain reaction primers. The products of the invention
 CC can be used in gene therapy and for treating cardiomyopathy, metabolic
 CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
 CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
 CC disease, immune disorders, haematopoietic disorders, and various
 CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
 CC syndrome X and wasting disorders associated with chronic diseases and
 CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments
 CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306
 XX
 SQ Sequence 928 AA;

Query Match 95.8%; Score 3093; DB 6; Length 928;
 Best Local Similarity 100.0%; Pred. No. 1.2e-307;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADREMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADREMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRKHILRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRKHILRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300

Db	241	FPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIE	TEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRR	MIRILKDLKQKHPEKDLDQLVEMANY	YALSHQQKSRAFYRIQATR 360
Db	301	LVPLEGKEVDESRR	MIRILKDLKQKHPEKDLDQLVEMANY	YALSHQQKSRAFYRIQATR 360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR		420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR		420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF		480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF		480
Qy	481	FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH		540
Db	481	FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH		540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV		595
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV		595

RESULT 12

ABB83247

ID ABB83247 standard; protein; 927 AA.

XX

AC ABB83247;

XX

DT 21-AUG-2002 (first entry)

XX

DE Human transporter protein-related protein, used in a homology alignment.

XX

KW Human; sodium/calcium exchanger; transporter; brain; heart; kidney; lung;

KW spleen; testis; leukocyte; foetal brain; chromosome 14.

XX

OS Unidentified.

XX

PN WO200233086-A2.

XX

PD 25-APR-2002.

XX

PF 17-OCT-2001; 2001WO-US032152.

XX

PR 17-OCT-2000; 2000US-0240836P.

PR 13-MAR-2001; 2001US-00804474.

XX

PA (PEKE) PE CORP NY.

XX

PI Merkulov GV, Ketchum KA, Shao W, Yan C, Di Francesco V;

PI Beasley EM;

XX

DR WPI; 2002-479677/51.

XX

PT Human transporter peptide related to sodium/calcium exchanger subfamily

PT for identifying modulators useful for treating a disease or condition

PT mediated by human transporter protein.

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGDLRDVPSAGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKLIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKLIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIA GD LGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIA GD LGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETR K I K H L R V F F I T A A W S I F A Y I W L Y M I L A V F S P G V V Q V W E G L L T L F F	240
Db	181	IIGICVYVIPDGETR K I K H L R V F F V T A A W S V F A Y I W L Y M I L A V F S P G V V Q V W E G L L T L F F	240
Qy	241	FPVCVLLAWVADKRLLFYKYM HK K Y R T D K H R G I I I E T E G D H P K G I E M D G K M M N S H F L D G N	300
Db	241	FPVCVLLAWVADKRLLFYKYM HK K R Y R T D K H R G I I I E T E G E H P K G I E M D G K M M N S H F L D G N	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKS RAF Y R I Q A T R	360
Db	301	LIPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKS RAF Y R I Q A T R	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENC GAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKTASMSEVHTDEPEDFASKVFFDPCSYQCLENC GAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF	480
Db	421	KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDEHF	480
Qy	481	FVRLSNVRIEEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRVEEEQLEEGMTPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 13

ABU12043

ID ABU12043 standard; protein; 895 AA.

XX

AC ABU12043;

XX

DT 19-FEB-2003 (first entry)

XX

DE Human NOV1c 248057963 protein SEQ ID 6.

XX

KW NOVX; human; antidiabetic; antiarteriosclerotic; anorectic; nootropic;

KW metabolic; antimicrobial; neuroprotective; antiparkinsonian; cardiant;

KW antilipaemic; cytostatic; immunomodulatory; gene therapy; dyslipidaemia;

KW cardiomyopathy; metabolic disorder; diabetes; atherosclerosis; obesity;

KW anorexia; neurodegenerative disorder; Alzheimer's disease; cancer;

KW Parkinson's disease; haematopoietic disorder; metabolic disturbance;

KW metabolic syndrome X; wasting disease.

XX

OS Homo sapiens.

XX

PN WO200281625-A2.

XX

PD 17-OCT-2002.

XX

PF 03-APR-2002; 2002WO-US010366.

XX

PR 03-APR-2001; 2001US-0281086P.

PR 05-APR-2001; 2001US-0281906P.

PR 06-APR-2001; 2001US-0282020P.

PR 10-APR-2001; 2001US-0282930P.

PR 12-APR-2001; 2001US-0283444P.

PR 12-APR-2001; 2001US-0283512P.

PR 13-APR-2001; 2001US-0283657P.

PR 13-APR-2001; 2001US-0283678P.

PR 13-APR-2001; 2001US-0283710P.

PR 17-APR-2001; 2001US-0284234P.

PR 19-APR-2001; 2001US-0285325P.

PR 20-APR-2001; 2001US-0285381P.

PR 24-APR-2001; 2001US-0286068P.

PR 25-APR-2001; 2001US-0286292P.

PR 07-JUN-2001; 2001US-0296692P.

PR 26-JUN-2001; 2001US-0300883P.

PR 08-AUG-2001; 2001US-0311003P.

PR 13-AUG-2001; 2001US-0311973P.

PR 16-AUG-2001; 2001US-0312901P.

PR 14-SEP-2001; 2001US-0322283P.

PR 05-OCT-2001; 2001US-0327448P.

PR 31-DEC-2001; 2001US-0345734P.

PR 03-JAN-2002; 2002US-0345755P.

PR 04-FEB-2002; 2002US-0354391P.

PR 02-APR-2002; 2002US-00114153.

XX

PA (CURA-) CURAGEN CORP.

XX

PI Padigar M, Shenoy SG, Kekuda R, Rastelli L, Mezes PD;

PI Smithson G, Guo X, Gerlach V, Casman SJ, Boldog FL, Li L;

PI Zerhusen BD, Tchernev VT, Gangolli EA, Vernet CAM, Spytek KA;
PI Malyankar UM, Patturajan M, Miller CE, Taupier RJ, Heyes MP, Ju J;
PI Peyman JA, Catterton E, Macdougall JR, Edinger SR, Stone DJ;
PI Mazur A;

XX

DR WPI; 2003-046862/04.

DR N-PSDB; ABX56263.

XX

PT New isolated NOVX polypeptide useful for treating cardiomyopathy,
PT atherosclerosis, metabolic disorders, diabetes, obesity, infectious
PT disease, anorexia, neurodegenerative disorders, Alzheimer's disease and
PT cancer.

XX

PS Claim 1; Page 86; 425pp; English.

XX

CC This invention describes novel polypeptides, termed NOVX which have
CC antidiabetic, antiarteriosclerotic, anorectic, metabolic, antimicrobial,
CC neuroprotective, antiparkinsonian, antilipaemic, cytostatic, nootropic,
CC cardiant and immunomodulatory activity. The polypeptide and any
CC antibodies generated from it are useful in the manufacture of a
CC medicament for treating a syndrome associated with a human disease
CC selected from a pathology associated with the NOVX polypeptide. Fragments
CC and portions of the polynucleotides encoding NOVX polypeptides are useful
CC to map the location of NOVX genes on a chromosome, to identify
CC individuals from minute biological samples, as DNA markers for
CC restriction fragment length polymorphism (RFLP), and are useful to
CC prepare polymerase chain reaction primers. The products of the invention
CC can be used in gene therapy and for treating cardiomyopathy, metabolic
CC disorders, diabetes, atherosclerosis, obesity, infectious disease,
CC anorexia, neurodegenerative disorders, Alzheimer's disease, Parkinson's
CC disease, immune disorders, haematopoietic disorders, and various
CC dyslipidaemias, metabolic disturbances associated with obesity, metabolic
CC syndrome X and wasting disorders associated with chronic diseases and
CC various cancers. ABU12041-ABU12086 represent the polypeptide fragments
CC encoded by the NOVX polynucleotides represented in ABX56261-ABX56306

XX

SQ Sequence 895 AA;

Query Match 91.1%; Score 2940; DB 6; Length 895;

Best Local Similarity 99.8%; Pred. No. 5.8e-292;

Matches 565; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 30 AEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL 89

:||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 2 SEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL 61

Qy 90 GVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEIL 149

||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 62 GVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEIL 121

Qy 150 LSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRRIKHLRVFFITA AW 209

||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 122 LSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRRIKHLRVFFITA AW 181

Qy 210 SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDK 269

||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 182 SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKYRTDK 241

Qy	270	HRGIIIEETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPE	329
Db	242	HRGIIIEETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPE	301
Qy	330	KDLQQLVEMANYALSHQOKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD	389
Db	302	KDLQQLVEMANYALSHQOKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD	361
Qy	390	EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDSKTMVVDYKTEDGSANAGADYEFT	449
Db	362	EPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDSKTMVVDYKTEDGSANAGADYEFT	421
Qy	450	EGTVVLKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP	509
Db	422	EGTVVLKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP	481
Qy	510	RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTV	569
Db	482	RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTV	541
Qy	570	EGTAKGGGEDFEDTYGELEFKNETV	595
Db	542	EGTAKGGGEDFEDTYGELEFKNETV	567

RESULT 14

AAE18291

ID AAE18291 standard; protein; 970 AA.

XX

AC AAE18291;

XX

DT 07-MAY-2002 (first entry)

XX

DE Bovine NCX-1 protein.

XX

KW Bovine; recombinant protein; larvae expression system; membrane protein;
 KW transport protein; cardiac sodium-calcium exchange protein; Na-K ATPase;
 KW NCX1; cystic fibrosis transmembrane conductance regulator; CFTR; vaccine;
 KW channel forming protein; junctional protein; connexin 32.

XX

OS Bos taurus.

XX

PN WO200206464-A2.

XX

PD 24-JAN-2002.

XX

PF 09-JUL-2001; 2001WO-US021606.

XX

PR 13-JUL-2000; 2000US-0218125P.

XX

PA (UMOR) UNIV MISSOURI.

XX

PI Hale CC, Price EM;

XX

DR WPI; 2002-171806/22.

DR N-PSDB; AAD24450.

XX Producing recombinant proteins e.g. membrane, transport and channel
PT forming proteins in larvae expression system, by infecting larvae with
PT vector having a sequence encoding recombinant fusion protein with
PT affinity tag.

XX

PS Example 1; Page 37-40; 40pp; English.

XX

CC The patent discloses methods of producing recombinant proteins in larvae
CC expression system, by infecting the larvae with vector having a sequence
CC encoding recombinant fusion protein with affinity tag. The methods are
CC useful for producing recombinant protein, preferably membrane proteins,
CC transport proteins such as NCX1 (cardiac sodium-calcium exchange protein)
CC or Na-K ATPase, channel forming proteins such as cystic fibrosis trans-
CC membrane conductance regulator (CFTR), junctional protein (connexin 32),
CC receptor, cytoskeletal and other membrane associated proteins. They are
CC also useful for producing prostate specific membrane antigens and sodium
CC phosphate co-transporters from kidney. The methods are also useful for
CC producing recombinant fusion proteins in large quantities that are both
CC highly homogenous and biologically active. The recombinant proteins
CC produced by the methods of the invention can be included as part of a
CC pharmaceutical, nutritional, drug or vaccine composition. The present
CC sequence is bovine NCX-1 protein

XX

SO Sequence 970 AA;

Qy	1	MAWLRLQLPTLSAFLHFLGLVTFVLF--LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV	58
Db	1	MLQFSLSPTLSMGFHVIAVMALLFSHVDHISAETEMEGEGETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN	118
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAAAFNM	178
Db	117	GETTTKTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAAFNM	176
Qy	179	FIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL	238
Db	177	FIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH	295
Db	237	FFFPICVVFVAVWADRRLLFYKYVYKRYRAGKQGRGMIIEHGEDRPSSKTEIEMDGKVNSH	296
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQ	348
Db	297	VDSFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355
Qy	349	KSRAFYRIQATRMMTGAGNILLKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSQC	407
Db	356	KSRAFYRIOATRLMTGAGNILLKRHAADOARKAVSMHEVNTEVAENDPVSKIFFEQGTQOC	415

Qy 408 LENC GAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
 |||| | ||::||:: ||::||::||::||::||::||::||::||::||::||::||::||
 Db 416 LENC GTVALTIIRRGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

Qy 468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
 ||||| ||||::| | ||||:: | |:: | | | | | | | | | | | | | | | | | |
 Db 476 IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVS---TLACLGSPSTATVTIFDDD 532

Qy 528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
 ||||| | |||||:||||| |||||: ||||: ||||: ||||| ||||
 Db 533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy 588 EFKNDETV 595
 ||: || |
 Db 593 EFQNDEIV 600

RESULT 15

AAM13701

ID AAM13701 standard; protein; 609 AA.

XX

AC AAM13701;

XX

DT 12-OCT-2001 (first entry)

XX

DE Peptide #135 encoded by probe for measuring cervical gene expression.

XX

KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer.

XX

OS Homo sapiens.

XX

PN WO200157278-A2.

XX

PD 09-AUG-2001.

XX

PF 30-JAN-2001; 2001WO-US000670.

XX

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX

DR WPI; 2001-488901/53.

XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human cervical epithelial cells.

XX

PS Claim 27; SEQ ID NO 18527; 487pp; English.

XX The present invention relates to human single exon nucleic acid probes
CC (SENP: see AAI10068-AAI28459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at [ftp.wipo.int/pub/published_pct_sequences](ftp:wipo.int/pub/published_pct_sequences)
XX
SQ Sequence 609 AA;

Query Match 66.4%; Score 2143.5; DB 4; Length 609;
Best Local Similarity 69.3%; Pred. No. 2.1e-210;
Matches 420; Conservative 76; Mismatches 89; Indels 21; Gaps 8;

Qy	1	MAWLRLQPLTSAFLHFGVLTFFVLF--LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEYV	58
Db	11	MRRLSLSPTFSMGFHLTVSLLFSHVDHVIAETEMEGEGETGE----CTGSYYCKKGV	66
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN	118
Db	67	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQKEITIKKPN	126
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCCHGFIAGDLGPSTIVGSAAFNM	178
Db	127	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCCHNFTAGDLGPSTIVGSAAFNM	186
Qy	179	FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL	238
Db	187	FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF	246
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKRYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH	295
Db	247	FFFPICVVFVAVVADRRLLFYKYVYKRYRAGKQRMIIIEHGEDRPSSKTEIEMDGKVNSH	306
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQ	348
Db	307	VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLSQQQ	365
Qy	349	KSRAFYRIQATRMMTGAGNILLKHAEEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYYQC	407
Db	366	KSRAFYRIQATRLMTGAGNILLKRAADQARKAVSMHEVNTEVTENDPVSKIFFEQGTYYQC	425
Qy	408	LENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLPKGETQKEFSVG	467
Db	426	LENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFVKPGDTQKEIRVG	485
Qy	468	IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD	527
Db	486	IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD	542
Qy	528	HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL	587
Db	543	HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL	602

Qy 588 EFKNDE 593
 ||:|||
Db 603 EFQNDE 608

Search completed: June 24, 2004, 16:11:58
Job time : 45.05 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2004, 16:09:57 ; Search time 15.6911 Seconds
 (without alignments)
 2039.888 Million cell updates/sec

Title: US-10-054-680-4
 Perfect score: 3228
 Sequence: 1 MAWLRLQPLTSAFLHFGLVT.....ADYGRGGQEDSRDGKASIG 620

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	362.5	11.2	539	4	US-09-701-068-2	Sequence 2, Appli
2	294.5	9.1	474	4	US-09-701-068-5	Sequence 5, Appli
3	113.5	3.5	339	4	US-09-134-001C-3608	Sequence 3608, Ap
4	108.5	3.4	652	1	US-08-050-684-2	Sequence 2, Appli
5	108.5	3.4	652	1	US-08-582-719-2	Sequence 2, Appli
6	106.5	3.3	501	4	US-09-489-039A-9817	Sequence 9817, Ap
7	105	3.3	404	4	US-09-198-452A-718	Sequence 718, App
8	103.5	3.2	988	2	US-08-286-819A-19	Sequence 19, Appl
9	103.5	3.2	988	3	US-08-980-357-19	Sequence 19, Appl
10	103	3.2	519	3	US-08-997-445D-2	Sequence 2, Appli
11	100.5	3.1	330	4	US-09-134-001C-3811	Sequence 3811, Ap

12	99.5	3.1	704	4	US-09-543-681A-7274	Sequence 7274, Ap
13	97.5	3.0	666	4	US-08-671-757A-13	Sequence 13, Appl
14	97.5	3.0	10182	4	US-09-134-001C-3159	Sequence 3159, Ap
15	96.5	3.0	429	4	US-09-107-532A-7193	Sequence 7193, Ap
16	94	2.9	583	4	US-09-328-352-6422	Sequence 6422, Ap
17	93	2.9	447	4	US-08-836-687B-39	Sequence 39, Appl
18	92.5	2.9	368	4	US-09-328-352-7684	Sequence 7684, Ap
19	92.5	2.9	1976	3	US-09-024-020B-9	Sequence 9, Appli
20	92.5	2.9	1976	4	US-09-425-043-9	Sequence 9, Appli
21	92.5	2.9	1978	3	US-09-024-020B-3	Sequence 3, Appli
22	92.5	2.9	1978	4	US-09-425-043-3	Sequence 3, Appli
23	92.5	2.9	1988	3	US-09-024-020B-4	Sequence 4, Appli
24	92.5	2.9	1988	4	US-09-425-043-4	Sequence 4, Appli
25	92	2.9	567	4	US-09-107-532A-6730	Sequence 6730, Ap
26	92	2.9	749	4	US-09-562-737-98	Sequence 98, Appl
27	92	2.9	911	4	US-09-489-039A-13537	Sequence 13537, A
28	91.5	2.8	382	4	US-09-252-991A-29696	Sequence 29696, A
29	91.5	2.8	503	4	US-09-562-737-67	Sequence 67, Appl
30	91.5	2.8	644	2	US-08-866-757-2	Sequence 2, Appli
31	91.5	2.8	644	3	US-09-153-593-2	Sequence 2, Appli
32	91	2.8	922	4	US-09-252-991A-32759	Sequence 32759, A
33	90.5	2.8	589	4	US-09-489-039A-12592	Sequence 12592, A
34	90.5	2.8	708	2	US-08-576-165-2	Sequence 2, Appli
35	90.5	2.8	1912	4	US-09-495-714C-2	Sequence 2, Appli
36	90.5	2.8	1977	4	US-09-495-714C-4	Sequence 4, Appli
37	90	2.8	497	3	US-09-058-947A-4	Sequence 4, Appli
38	90	2.8	500	4	US-08-868-373-12	Sequence 12, Appl
39	90	2.8	548	3	US-08-656-034-10	Sequence 10, Appl
40	90	2.8	594	4	US-09-107-532A-7250	Sequence 7250, Ap
41	90	2.8	612	4	US-09-252-991A-17516	Sequence 17516, A
42	90	2.8	628	3	US-08-656-034-2	Sequence 2, Appli
43	90	2.8	1003	4	US-09-198-452A-17	Sequence 17, Appl
44	89.5	2.8	1052	3	US-09-255-502-7	Sequence 7, Appli
45	89.5	2.8	1052	4	US-09-360-237-3	Sequence 3, Appli

ALIGNMENTS

```

RESULT 1
US-09-701-068-2
; Sequence 2, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 539
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana

```

US-09-701-068-2

Query Match 11.2%; Score 362.5; DB 4; Length 539;
Best Local Similarity 31.3%; Pred. No. 3e-28;
Matches 91; Conservative 61; Mismatches 96; Indels 43; Gaps 9;

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Qy      64 YPENPSLGDKIARVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIKKPNGETST 123
      :|  :|  | : | ::||: | | |:|:| | || |:| :   |:|   | :
Db      29 FPGENTLSDGL-RGVLYFLGLAYCFIGLSAITARFFKSMENVVKHSRKVVTIDPITKAEV 87

Qy      124 TTI-RVWNETVSNLTLMALGSSAPEILLSLIEV---CGHGFIAGDLGPSTIVGSAAFNMF 179
      | :||| |:::~:| | :| | :| | : | :   | : || ||| |:|||||:~:|
Db      88 ITYKKVWNFTIADISLLAFGTSEFPQISLATIDAIRNMGERY-AGGLGPGTLVGSAAFDLF 146

Qy      180 IIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLF 239
      | :|| |  || :|| | | : :  || :|||||:~:| |:|| | : : | |||:
Db      147 PIHAVCVVVPKAGELKKISDLGVWLVELVWSFWAYIWLYIILEVWSPNVITLVEALLTVL 206

Qy      240 FFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDG 299
      : : : : | : |||  : | :   : : || | :
Db      207 QYGLLLVHAYAQDKR---WPYLS-----LPMSRGDRPE----- 236

Qy      300 NLVPLEGKEVDESR----REMIRILKDLKQKHPEKDLDQLVEMANYALSH 346
      ||  :|:| | :   : : : | | |  :|:~: : : : :
Db      237 EWVP---EEIDTSKDDNDNDVDVYSDAAQDAVESGSRNIVDIFSISANN 284
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RESULT 2

US-09-701-068-5

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; Sequence 5, Application US/09701068
; Patent No. 6677506
; GENERAL INFORMATION:
; APPLICANT: Galil, Gad et al.
; TITLE OF INVENTION: DNA CODING FOR A Mg2+/H+ OR Zn2+/H+ EXCHANGER AND
TRANSGENIC PLANTS
; TITLE OF INVENTION: EXPRESSING SAME
; FILE REFERENCE: 01/21317
; CURRENT APPLICATION NUMBER: US/09/701,068
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-701-068-5
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Query Match 9.1%; Score 294.5; DB 4; Length 474;
Best Local Similarity 30.7%; Pred. No. 2.5e-21;
Matches 79; Conservative 52; Mismatches 73; Indels 53; Gaps 9;

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Qy      97 RFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEV- 155
      | : :|| | | :| ||           ||| |:::~:| | :| | :| | :
Db      9  RKVVTIDPITKAE-VITYKK-----VWNFTIADISLLAFGTSEFPQISLATIDAI 56

Qy      156 --CGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFA 213
      | : || ||| |:|||||:~:| | :|| |  || :|| | | : :  || :|
```

```

Db          57 RNMGERY-AGGLPGGTLVGSAAFDLFPIHAVCVVVPKAGELKKISDLGVWLVELVWSFWA 115
Qy          214 YIWLYMILAVFSPGVVQVWEGLLTLFFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGI 273
          |||||:| | :| | | : | ||| : : : : | : ||| : | :
Db          116 YIWLYIILEVWSPNVITLVEALLTVLQYGLLLVHAYAQDKR---WPYLS----- 161
Qy          274 IIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESR---REMIRILKDLKQKHPE 329
          : : || | : || : || : | : : : | | | |
Db          162 LPMSRGDRPE-----EWVP---EEIDTSKDDNDNDVHDVYSDAQAQDAVE 202
Qy          330 KDLDQLVEMANYYALSH 346
          :| : : : : :
Db          203 SGRNIVDIFSIHSANN 219

```

RESULT 3

US-09-134-001C-3608

; Sequence 3608, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3608

; LENGTH: 339

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3608

Query Match 3.5%; Score 113.5; DB 4; Length 339;

Best Local Similarity 20.4%; Pred. No. 0.0072;

Matches 69; Conservative 53; Mismatches 149; Indels 67; Gaps 12;

```

Qy          195 RKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFFPVCVLLAWVADKR 254
          |||| : | : : | | | : : | : || | : | | : : |
Db          3 RKIKRSDLMF-SIGFIIIAVIIIVALLILFSFVPGVLWISALAA---GVHVGIGTLVGMR 58
Qy          255 LLFYKYMHHKKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFL-----DGNL----- 301
          | | | | | : | | | : : : | : | : | : |
Db          59 L-----RRVSPRKVIAPLIKAHAGLNLTTNQLESHYLAGGNVDRVVDANIAAQR 108
Qy          302 -----VPLE-GKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRIFYRI 356
          : | | | : | : | : : : : : : : : : : |
Db          109 ADIDLPPFERGAIDLGRDVLVAVQ--MSVNPKVIETPFIAGVAMNGIEVKAKARITVRA 166
Qy          357 QATRMMTGAG-NILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSQCLENCGAVL 415
          | : : ||| : | | | | | : | : | :
Db          167 NIARLVGGAGEETIARVGEIVSTIGSSEHHT-----EVLENPDNIS 209

```

Qy 416 LTVVRKG---GDMSKTMVVDYKTEDGSANAGADYE----FTEGTVVLKPGETQKEFSVGI 468
 ||: || | : : :| | | ||| : : : | : : |
 Db 210 KTVLSKGLDSGTAFEILSIDIADVDISKNIGADLQTEQALADKNIAQAKAEERRAMAVA- 268
 Qy 469 IDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSL 506
 :: | : : | : : | : | : | : |
 Db 269 -----SEQEMKARVQEMRAKVVEAESEVPLAMAEAL 299

RESULT 4

US-08-050-684-2

; Sequence 2, Application US/08050684
 ; Patent No. 5550221
 ; GENERAL INFORMATION:
 ; APPLICANT: Johann Dr., Stephen V.
 ; APPLICANT: Van Zeijl Dr., Marja
 ; APPLICANT: O'Hara Dr., Bryan M.
 ; TITLE OF INVENTION: Amphotropic Virus Receptor
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: American Cyanamid Company
 ; STREET: 1937 West Main Street
 ; CITY: Stamford
 ; STATE: CT
 ; COUNTRY: United States of America
 ; ZIP: 06904-0060
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/050,684
 ; FILING DATE: 16-APR-1993
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lowney Dr., Karen A
 ; REGISTRATION NUMBER: 31,274
 ; REFERENCE/DOCKET NUMBER: 31937-00
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 203-321-2361
 ; TELEFAX: 203-321-2971
 ; TELEX: 710-474-4059
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 652 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-050-684-2

Query Match 3.4%; Score 108.5; DB 1; Length 652;
 Best Local Similarity 19.9%; Pred. No. 0.072;
 Matches 124; Conservative 89; Mismatches 210; Indels 201; Gaps 30;

Qy 77 VIVYFVALIYMF-LGVSIADRFMASI--EVITSQER-----EVTIKKPNGET- 121


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      :: : : | | : | : : : | : : | : | : :
Db      11 ILGFIIAFILAFSVGANDVANSFGTAVGSGVVTLRQACILASIFETTGSVLLGAKVGETI 70

Qy      122 --STTTIRVWNETVSNLTLMA-----LGSSAPEILLSLIE--VCG-HGFIAGDLGPSTI 170
      : : : | | | | | : : : | : : | : : | : :
Db      71 RKGIIIDVNLNETVE--TLMAGEVSAMVGSVWQLIASFLRLPISGTHCIVGSTIGFSLV 128

Qy      171 V-----GSAAFNMFIIGICVYVIPDGETRKHHLRVFF- 204
      | : : : | | : | : : | | :
Db      129 AIGTKGVQWMELVKIVASWFISPLLSGFMSSGLLFVLIRIFILKKEDVPVNGLRALPVFYA 188

Qy      205 ITAAWSIFAYIW-----LYMILAVFSPGVVQVWEGLLTLFFFFPVCV----- 245
      | | : : | : : | : : : : | | | : |
Db      189 ATIAINVFSIMYTGAPVLGLVLPWMAIALISFGVALLFAFFVWLFVCPWMRRKITGKLQK 248

Qy      246 --LLAWVADKRL-----LFYKYMHHKYRTDKH---RGIIEET-----EGDHPK 283
      | : | : | : | : | : | : | : | : | :
Db      249 EGALSRVSDSLSKVQEAESPVKELPGAKANDDSTIPLTGAAGETLGTSEGTSAGSHPR 308

Qy      284 GI-----EMDGKMMNSHF-----LDGNLVPLEGKEVDESRRMIRILKDLKQK 326
      : : | | | : : | : : : : | : | :
Db      309 AAYGRALSMTHGSKSPI SNGTFGFDGHTRSDGHVYHTVHKDSG-----LYKDLLHK 360

Qy      327 -HPEKDLDQLVEMANYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSE 385
      | : : : : | : | : | : | : | : | :
Db      361 IHIDRGPEEKPAQESNYRLRRNNSYTCY----TAAICG----LPVHATFRAADSSA--- 409

Qy      386 VHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGAD 445
      | | | | : | | | : | : | : : | | :
Db      410 -----PED-SEKLVGDTVSYSS-----KKRLRYDSYSSYCNVAEAE 444

Qy      446 YEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPA--IF 503
      | | | : | : : | | | | : | : | : |
Db      445 IEAEEGGVEMK-----LASELADPDQPREDP-----AEEEEKEEKDAPEVHLLF 487

Qy      504 NSLPLPRAVLAS-----PCVATVTILDDDHAGIFTFECDT-----IHV 541
      : | : | | | | | | | | | | : :
Db      488 HFLQVLTACFGSFAHGGNDVSNAIGPLVALWLIYKQ---GGVTQEATPVWLLFYGGVGI 544

Qy      542 SESIGVMEVKVLRITSGARGTVVIP 565
      : | : : : | | |
Db      545 CTGLWVWGRRVIQTMGKDLTPITP 568

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RESULT 5

US-08-582-719-2

; Sequence 2, Application US/08582719

; Patent No. 5633348

; GENERAL INFORMATION:

; APPLICANT: Johann Dr., Stephen V.

; APPLICANT: Van Zeijl Dr., Marja

; APPLICANT: O'Hara Dr., Bryan M.

; TITLE OF INVENTION: Amphotropic Virus Receptor

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: American Cyanamid Company

; STREET: 1937 West Main Street


```

      :  : | |      ||::  :      : || | |
Db      309 AAYGRALSMTHGSKVSPISNGTFFGDFDGHTRSDGHVYHTVHKDSG-----LYKDLLHK 360
QY      327 -HPEKDLQQLVEMANYALSHQQKSRFYRIQATRMMTGAGNILKKHAAEQAKKASSMSE 385
      | :: ::      : | | : | |      | : |      | | : | : | :
Db      361 IHIDRGPEEKPAQESNYRLLRRNNSYTCY----TAAICG----LPVHATFRAADSSA--- 409
QY      386 VHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGAD 445
      |||  | : | ||      | : | : : | | | :
Db      410 -----PED-SEKLVGDTVSYSS-----KKRLRYDSYSSYCNAAVEAE 444
QY      446 YEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPA--IF 503
      | | | : |      : : | | ||      ||| : | : | : |
Db      445 IEAEEGGVEMK-----LASELADPDQPREDP-----AEEKEEKDAPEVHLLF 487
QY      504 NSLPLPRAVLAS-----PCVATVTILDDDHAGIFTFECDT-----IHV 541
      : | : | |      | || |      | | |      : :
Db      488 HFLQVLTACFGSFAHGGNDVSNAIGPLVALWLIYKQ---GGVTQEAATPVWLLFYGGVGI 544
QY      542 SESIGVMEVKVLRTSGARGTVIVP 565
      : | : | : | | | |
Db      545 CTGLWVWGRRVIQTMGKDLTPITP 568

```

RESULT 6

US-09-489-039A-9817

; Sequence 9817, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 9817

; LENGTH: 501

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-9817

Query Match 3.3%; Score 106.5; DB 4; Length 501;

Best Local Similarity 19.8%; Pred. No. 0.074;

Matches 82; Conservative 66; Mismatches 156; Indels 111; Gaps 16;

```

QY      61 PIWYPENPSLGDKIARVIVYFVALIYMFGLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
      | | | | | | | : | | | | : | | : | | : | : | : | :
Db      146 PDWLTCNP-----APVVNQNDAVIYYFFRNIMMAVLFMSSIILYYFRQIRIMHSWKAHVL 199
QY      121 TSTTTIRVWNETVSNLTLMAL----GSSAPEILLSLIEVCGHGFIAGDLGP--STIVGSA 174
      | | | : | : | | : | : : | | : | : | : | :
Db      200 TFTACI-----LFTLTIIVLSWLYSSHSPWLSVNFIDDLSTFT-----PLWQSIIGWL 248

```

```

Qy      175 AFNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVW-- 232
      : : | | : : | : : : | : | : : | |
Db      249 LMAVWFITLILLISLS-----KLRNIFWFSGAFFCSAYLFTLFQLLSTAGELDQTWYQ 301

Qy      233 ----EGLLTFFFPPVCVLLAWVADKRLLF----YKYM-----KKYRTDK 269
      | | ||| : : | : : : | : | : : |
Db      302 ARFFETLCTLF-----LILVLLVDVFILYRESNHKYVHSYQNSIRDPLTRLNRSFFYDT 356

Qy      270 HRGIIIEGEGDHPKGI---EMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQK 326
      : : | | : : | | | : : | :
Db      357 LNQQLAQVNAQHPLSVLISDLD-----HF-----KRINDSYGHVAG----- 392

Qy      327 HPEKDLQVLVEMANYALSHQQKSRIFYRI---QATRMGTGAGNILKKHAAEQAKKASSM 383
      | : : : | | : | | : : | : | : : |
Db      393 -----DKVIQFAASVLESHSRVDDAAARIGGEFALLVNTGEKEAQAIAERIRLAVSA 446

Qy      384 SEVHTDEPEDFISKVF-----FDPCSYQCLENCGAVLLTVVRKGG 423
      | | | : : | : | : : | : |
Db      447 GESHLPERMTISMGVYTTHDNSVTAEACVQRADEAMYEAKNNGRNQVIVWHRQGG 501

```

RESULT 7

US-09-198-452A-718

; Sequence 718, Application US/09198452A

; Patent No. 6559294

; GENERAL INFORMATION:

; APPLICANT: Griffais, R.

; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention

; TITLE OF INVENTION: and treatment of infection

; FILE REFERENCE: 9710-003-999

; CURRENT APPLICATION NUMBER: US/09/198,452A

; CURRENT FILING DATE: 1998-11-24

; NUMBER OF SEQ ID NOS: 6849

; SEQ ID NO 718

; LENGTH: 404

; TYPE: PRT

; ORGANISM: Chlamydia pneumoniae

US-09-198-452A-718

Query Match 3.3%; Score 105; DB 4; Length 404;

Best Local Similarity 21.5%; Pred. No. 0.073;

Matches 79; Conservative 51; Mismatches 154; Indels 84; Gaps 15;

```

Qy      265 YRTDKHRGIIIEGEGDHPKGIEMDGKMMNSHFLD-----GNLVPLEGKEVDESRRMIR 318
      | | | : : : | | : : | : | | | : :
Db      48 YLLKKHAAVILMSHLGRPKGQGFQEEYSLQPVDVLEGYLGHHVPLAPDCVGEVARQAVA 107

Qy      319 -----ILKDLK-----QKHPEKDLQVLVEMANY-----YALSHQQKSRIFYRIQA 358
      : : : : : : | : : | : | : : : |
Db      108 QLSPGRVLLLENLRFHIGEEHPEKDPTFAAELSSYGDFYVNDAFGTSHRKHASVYVVPQA 167

Qy      359 TRMTGTGAGNILKK-----HAAEQAKK-----ASSMSEVHTDEPEDFISKVFFDPC 403
      | | : : | | : | : | : : : :
Db      168 FPGRAAAGLLMEKELEFLGRHLLTSPKRPFTAILGGAKISSKIG-----VIEALLNQV 220

```

Qy 404 SYQCLENCGAVLLTVVRKGGDSMTMYVDYKTEDGSANAGADYEFTEGTVVL----KPGE 459
 | | | : | :: | | : | : | : | : | | |
 Db 221 DYLLL--AGGMGFTFLQALGKSLGNSLVEKSALDLARNVLKIAKSRNVTIVLPSDVKAAE 278
 Qy 460 T--QKEFSVGIIDD-----DIFEEDEHFFVRLSN-----VRIEEEQPEEGM 498
 ||: || || || || ||: | : | : | :
 Db 279 NLQSKEYSVISIDQGIPPHLQGFDIGPRTTEEFIRIINQSATVFWNGPVGVE-----V 332
 Qy 499 PPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDT--IHVSESIGVMEVKVLRIS 556
 || | : : | : | | | : | | || | : : |
 Db 333 PPFDSGSIAIANALGNHPSAVTVVGGGDAAAVVALAGCSTKVSHVSTG--GGASLEFLEQG 391
 Qy 557 GARGTVIV 564
 | : :
 Db 392 FLPGTEVL 399

RESULT 8

US-08-286-819A-19

; Sequence 19, Application US/08286819A

; Patent No. 5871910

; GENERAL INFORMATION:

; APPLICANT: ARTHUR, MICHEL

; APPLICANT: DUKTA-MALEN, SYLVIE

; APPLICANT: MOLINAS, CATHERINE

; APPLICANT: COURVALIN, PATRICE

; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE

; TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR

; TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR

; TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

; NUMBER OF SEQUENCES: 54

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. Jefferson Davis Highway, Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/286,819A

; FILING DATE: 05-AUG-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/174,682

; FILING DATE: 28-DEC-1993

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/917,146

```

; FILING DATE: 10-AUG-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR/91/00855
; FILING DATE: 29-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9013579
; FILING DATE: 31-OCT-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5871910man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-060-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 988 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-286-819A-19

```

```

Query Match          3.2%; Score 103.5; DB 2; Length 988;
Best Local Similarity 19.3%; Pred. No. 0.48;
Matches 116; Conservative 89; Mismatches 173; Indels 223; Gaps 32;

```

```

Qy      3 WLRLQPLTSAFLHFGLVTFVL-----FLNGLRAEAGGSGDVPSTGQNNESCSGSSDC 54
      | | : : | : || | : | : | : | : | : | : | : | : | : | : | : |
Db      104 WDHLKEIRS---EYDFVTFTLSEYRMTFKYLHQLALE-----NGDAIHLHLEC 148

Qy      55 -----KEGVILP-----IWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMAS 101
      | : || | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      149 IDFLRKNKIILPAITTLERMVW--EARAMAEK-----KLFNTVS----- 185

Qy      102 IEVITSQERE-----VTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVC 156
      : : | : : : | : | : | : | : | : | : | : | : | : | : | : |
Db      186 -KSLTNEQKEKLEGIITSQHPS--ESNKTILGWLKEPP-----GHPSPETFLKIIE-- 233

Qy      157 GHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKKIKHL---RVFFITA----- 207
      : | | : | | : | | : | | : | : | : | : | : | : | : | : | : |
Db      234 -----RLEYIRGM-----DLETVQISHLHRNRLQLSRLGSRYE 267

Qy      208 --AWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKY 265
      | : | | | : : : : | : | : | : | : | : | : | : | : | : |
Db      268 PYAFRDFQENKRYSIILTIY---LLQLTQELTDKAF-----EIHDRQILSLLSKGRKA 316

Qy      266 RTDKHRGIIIEGTHPKGIEMDGKMMNS---HFLDGNLVPLEGKEVDESRRMIRILKD 322
      : : : : : | : | : | : | : | : | : | : | : | : | : | : |
Db      317 QEEIQK-----QNGKKLNEKVIHFTN-----IGQALIKAREEKLDVFKV 355

Qy      323 LKQ-----KHPEKDLQVLVEMANYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAE 375
      | : : : : | : | : | : | : | : | : | : | : | : | : | : |
Db      356 LESVIEWNTFVSSVEEAQELARPADYDYDLLQK--RFYSLR--KYTPTLRLRVLEFHSTK 411

```

Qy 376 -----QAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVL----- 415
: | :| | | | | : | :
Db 412 ANEPLLQAVEIIRGMNESGKRKVPDDSPVDFISKRW----KRHLYEDDGT TINRHHYEMA 467
Qy 416 -LTVVR---KGGDMS---KTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGI 468
|| :| : ||:| | |:: :| |::| | :| :
Db 468 VLTELREHVRAGDVSIVGSRQYRDFE-----EYLFSEDTWNQSKGNTRLSVSL- 516
Qy 469 IDDDIFEDEHFFVR-----LSNVRIEEEQPEEG--MPPAIFNSL 506
:| | | | | || |::: || :::|
Db 517 FEDYITERTSSFNERLKWLAANSNKLDGVSLEKGLSLARLEKDVPEEAKKFSASLYQML 576
Qy 507 P 507
|
Db 577 P 577

RESULT 9

US-08-980-357-19

; Sequence 19, Application US/08980357

; Patent No. 6013508

; GENERAL INFORMATION:

; APPLICANT: ARTHUR, MICHEL

; APPLICANT: DUKTA-MALEN, SYLVIE

; APPLICANT: MOLINAS, CATHERINE

; APPLICANT: COURVALIN, PATRICE

; TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE

; TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR

; TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR

; TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS

; NUMBER OF SEQUENCES: 54

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. Jefferson Davis Highway, Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/980,357

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/286,819

; FILING DATE: 05-AUG-1994

; APPLICATION NUMBER: US 08/174,682

; FILING DATE: 28-DEC-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/917,146

```

; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR/91/00855
; FILING DATE: 29-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9013579
; FILING DATE: 31-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 6013508man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-060-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 988 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-980-357-19

```

```

Query Match          3.2%; Score 103.5; DB 3; Length 988;
Best Local Similarity 19.3%; Pred. No. 0.48;
Matches 116; Conservative 89; Mismatches 173; Indels 223; Gaps 32;

```

```

Qy      3 WLRQLPLTSAFLHFGVLTFVL-----FLNGLRAEAGGSGDVPSTGQNNESCSGSSDC 54
      | | : : | : || | : | : | | : : : |
Db     104 WDHLKEIRS---EYDFVTFTLSEYRMTFKYLHQLALE-----NGDAIHLLHEC 148

Qy      55 -----KEGVILP-----IWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMAS 101
      | : || | : | | : : : | : | |
Db     149 IDFLRKNIILPAITTLERMVW--EARAMAEK-----KLFNTVS----- 185

Qy     102 IEVITSQERE-----VTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVC 156
      : : | : : | : | : | : | | : | : | | : | |
Db     186 -KSLTNEQKEKLEGIITSQHPS--ESNKTILGWLKEPP-----GHPSPETFLKIIE-- 233

Qy     157 GHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRRIKHL---RVFFITA----- 207
      : | | : | | : | | | : :
Db     234 -----RLEYIRGM-----DLETVQISHLHRNRLQLSRLGSRYE 267

Qy     208 --AWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKY 265
      | : | | | : : : : | : | : : | : |
Db     268 PYAFRDFQENKRYSIILTIY---LLQLTQELTDKAF-----EIHDRQILSLLSKGRKA 316

Qy     266 RTDKHRGIIIEGTEGDHPKGIEMDGKMMNS---HFLDGNLVPLEGKEVDESRRMIRILKD 322
      : : : : | | : | | : | : : : | : : |
Db     317 QEEIQK-----QNGKKLNEKVIHFTN-----IGQALIKAREEKLDVFKV 355

Qy     323 LKQ-----KHPEKDLDQLVEMANYALSHQQKSRAFYRIQATRMGTGAGNIIKKHAAE 375
      | : : : | : | | | : : : : | : : :
Db     356 LESVIEWNTFVSSVEEAQELARPADYDYDLLQK--RFYSLR--KYTPTLRLRVLEFHSTK 411

Qy     376 -----QAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVL----- 415
      : | : | | | | : | :

```


Query Match 3.2%; Score 103; DB 3; Length 519;
Best Local Similarity 20.7%; Pred. No. 0.18;
Matches 47; Conservative 44; Mismatches 90; Indels 46; Gaps 10;

```

Qy      282 PKGIEMDGKMMNSHFLDGNLVPLEGKEVDESREMI-----RIL-----KDLKQKH 327
      |::| | : : | :|: : |:|:: | : |:: | : ::|
Db      165 PQGVAMRAGVL----ADDHLIEVNGENVEDASHEKVVEKVKKSGSRVMFLLVDKETDKRH 220

Qy      328 PEKDLQDLVEMANYALSHQQKSRAFYRIQATRMGTAGNILKKHAAEQAKKASSMSEVH 387
      |: : | |: | | : : : | | |: | : | : :
Db      221 VEQKIQFKRETASLKLLPHQPRI-----VEMKKGSNGYGFYLR---AGSEQKGQIIKDID 272

Qy      388 TDEP-----EDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGS 439
      : | | : | : | :|:: | :||| | : : || :|:
Db      273 SGSPAEEAGLKNNDLVAVNGE--SVETLDHDSVV--EMIRKGGDQTSLLVVDKETDNMY 328

Qy      440 ANAG-----ADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEEDH 479
      | | | | | | | | | | | | | | | |
Db      329 LRAHFSPFLYYQSQELPNGSVKEAPAPTPTSLEVS-SPPDTTEEVDH 374

```

RESULT 11

US-09-134-001C-3811

; Sequence 3811, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3811

; LENGTH: 330

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3811

Query Match 3.1%; Score 100.5; DB 4; Length 330;

Best Local Similarity 21.8%; Pred. No. 0.15;

Matches 47; Conservative 32; Mismatches 88; Indels 49; Gaps 6;

```

Qy      302 VPLEGKEVDESRRMIRILKDLKQKHPEKDLQDLVEMANYALSHQQKSRAFYRIQ--AT 359
      | : ||: |: :: || :| | :|: | | : : ||
Db      135 VNVSDKEIKENSKKTSILIKVKSXSDDKE-----GLSDKKAKEKAKEKIQKEVE 183

Qy      360 RMTGAGNILKKHA--AEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLT 417
      : | | | | : : ||| |: | : | | |
Db      184 KNPKNKFGELAKKESMDSSSAKKGDSLGYVIKQMVDSEKALFK----- 227

Qy      418 VVRKGGDMSKTMVVDY-----KTEDGSANAGADYEFTEGTVVLKP-----GETQ 461
      | |::|| : || :|: | : : | | || |
Db      228 --LKEGEVSKVVKTDYGYHIIKADKETDFNSEKSNIKQKLIIEKVQKKPKLLTDAYKELL 285

```

Qy 462 KEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEG 497
 ||: | | | : | : : : : | : |
 Db 286 KEYKVDYKDRDIKKAIEDSILDPDKIKQQQQQQSQG 321

RESULT 12

US-09-543-681A-7274
 ; Sequence 7274, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS
 MIRABILIS FOR
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 7274
 ; LENGTH: 704
 ; TYPE: PRT
 ; ORGANISM: Proteus mirabilis
 US-09-543-681A-7274

Query Match 3.1%; Score 99.5; DB 4; Length 704;
 Best Local Similarity 17.1%; Pred. No. 0.69;
 Matches 113; Conservative 94; Mismatches 186; Indels 269; Gaps 32;

Qy 9 LTS AFLH FGLVTFVLFL---NGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYP 65
 | | : | : | | | | : | : | : | : | : |
 Db 116 LVVGFVVFVSIVTIVQFLVITKGSERVAEVAARFSLDGM PGKQMSIDADLKSGII----- 169

Qy 66 ENPSL-----GDKIARVIVYFVALIYMFLGVSIADRFMA 100
 | : || || : : || || | : :
 Db 170 TNEEVQIRRKELGQESQLYGSFDGAMKFIKGD A IAGIV IIFVN LIG---GISVGMAQMGL 226

Qy 101 SIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALG---SSAPEILLSLIEVC 156
 || | : || : | : | : | : | :
 Db 227 SI-----TEALHTYTLTIGDGLVAQIPALLISI---- 255

Qy 157 GHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETR KIKHLRVFFITAAWSIFAYIW 216
 ||| : | || : : : : | :
 Db 256 SAGFIVTRVG-----GENNNLGY-----SIMNELLAQDF 284

Qy 217 LYMILAV-----FSPG----VVQVWEGLLTLFFFPVCVLLAWVADKRLLEFYKYM HKKYR 266
 : : | : | | | : : | : : | : | : :
 Db 285 ALLVTAILAFGIGFLPGFPTPVFLILSVMLGVYFFKI----KWKSSK-----KEYK 331

Qy 267 TDKHRGII IETEGDHPKGI-----EMDGKMM--NSHFLDGNLVPL----- 304
 | : : | | || : | : : | : ||
 Db 332 TEDEKDNHNATNADSKKGLMSNLFSGKHGEEVDNSLLTENITLSQAETLPLIITLSTK K 391

Qy 305 -----EGKEVDESRRREMIRILKDLKQK----- 326
 : : : : : | : : : |
 Db 392 PYLTKIVFEKWLQKEFILQYGILLPDI VIHYSDKIDDDK--IIILINEVKAKELNCPFPPL 449

Qy 327 -HPEKDL DQLVEMA-----NYALSHQOKSRA-----FYR----- 355
 | | | : : : : : | | |
 Db 450 FH IENPNDELLSLGFNLISIEDDNKTHYWI ERDDESKLAPLG YKAERSESYFYRKFS DLI 509
 Qy 356 -----IQATRM MTGAGN ILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQ 406
 | | | : : : | : | | | : : | : : :
 Db 510 TLNITEFLGIQETKDIL---DKLEKSAPELLKEC--YRQVSIQRINDVLQRLVQEKIP-- 562
 Qy 407 CLENCGAVLLTVVRKGG-----DMSKTM---YVDY-KTEDGSANA---GADYE--- 447
 : | : : : | : : | : | : | | | |
 Db 563 -IRNIKTIIGGLVQWGSKEKDPVLLTEHIRTLLARYISYFFSTDGKFNAIILSNDMEEII 621
 Qy 448 -----FTEGTVV-LKPGETQKEF-SVGIIDDDIFEDEHFFVRLSNVR-----IEEEQ 493
 : | : : | : | : : | | : : | : : | :
 Db 622 RSGIRQSSSGTLLNLEPAELDMIIEKISMVIDDIKYIQDYIFLT SIDIRRFVKKLIETQY 681
 Qy 494 PE 495
 | :
 Db 682 PQ 683

RESULT 13

US-08-671-757A-13

; Sequence 13, Application US/08671757A

; Patent No. 6476213

; GENERAL INFORMATION:

; APPLICANT: Suerbaum, Sebastian

; TITLE OF INVENTION: Cloning and Characterization Production
 ; of Aflagellate Strains

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 ; Dunner

; STREET: 1300 I Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20005-3315

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/671,757A

; FILING DATE: 16-Aug-2001

; CLASSIFICATION: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Meyers, Kenneth J.

; REGISTRATION NUMBER: 25,146

; REFERENCE/DOCKET NUMBER: 02356.0073-00000

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 408-4000

; TELEFAX: (202) 408-4400

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

```

;           LENGTH: 666 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;           MOLECULE TYPE: peptide
;           SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-08-671-757A-13

```

```

Query Match           3.0%; Score 97.5; DB 4; Length 666;
Best Local Similarity 20.8%; Pred. No. 1;
Matches 128; Conservative 83; Mismatches 210; Indels 193; Gaps 33;

```

```

Qy      9 LTS AFLH FGLVT---FVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYP 65
      |  | : | : ||  |::  |  | :  |  | : | | | : |
Db      91 LAVGFVIFSIVTVVQFIVITKGSERVAEVAARFSLDGM PGKQMSIDADLKAGIIDAAGAK 150

Qy      66 ENPSL-----GDKIARVIVYFVALIYMFLGVSI IADRFMASIEVIT 106
      |  | :  |  | | | | : | | |  | : | :  |  | :
Db      151 ERRSILERESQLYGSFDGAMKF IKGDAIAGIIIFVNLIG---GISVGMSQHGM SL---- 203

Qy      107 SQEREVTIKKPNGETSTTTIRVWNETVSNLTL-MALGSSAPEILLSLIEVCGHGF----I 161
      : |  | | |  | | :  |  |  | : | :  |  | :
Db      204 -----SGALSTYTI-----LTIGDGLVSQIPALLISI-----SAGFMLTRV 239

Qy      162 AGD---LGPSTIVGSAAFNMFIIGICVYVIPDGETR KIKHLRVFFITAAWSIFAYIWLY 218
      ||  : |  | :  | | : |  |  | : | :
Db      240 NGDSDNMG-RNIMSQIFGNPFVLI-----VTSA----- 266

Qy      219 MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRL LFYKYMHKKYRTDKHRGIIETE 278
      : || :  | : |  | | | | : |  |  | : | :  | : :
Db      267 LALAI-----GMLPGFPFFVF FLIA-VTLTALFYKKV-----VEKEKSLS ES DS 310

Qy      279 GDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRR EMI-RILKDLKQKHPEKDLDQLVE 337
      :  : : |  | : |  | : |  | :  |  | :  |  | : : | : |
Db      311 SGYTGTFDID-----NTH--DSSLAMIE--NLDRI SSETVPLILLFAENKINANDMEGLIE 362

Qy      338 MANYYALSHQQKSRAF--YRIQATRM MTGAGN ILKKHAAEQAKKASSMSEVHTDEPEDFI 395
      : : | :  |  | : :  |  |  |  |  | : : |  | :
Db      363 -----RIRSQFFIDYGVRLPTILYRTSNE LKVDDI-----VLLINEVRADSFNIYF 408

Qy      396 SKVFFDPCSYQCL--EN--CGAVLLTVVRKGGDMSK TMYVDYKTEDGSANAGADYEFTEG 451
      ||  | :  | |  | : : | |  :  : | |  :  |  | : :
Db      409 DKV-----CITDENG DIDALGIPV VSTS YNERVISWVDVSYTENLTNIDAKIKSAQ- 459

Qy      452 TVVLKPGETQKEFSVGIIID--DDIF-----EED E HFFV-RLSNV 487
      |  :  |  : :  | : : |  |  |  | : | : | |
Db      460 -----DEFYHQLSQALLNNINEIFGIQETKNMLDQFENRYPDLLKEVFRHV TIQRISEV 513

Qy      488 --RIEEEQPEEGMPPAIFNSLPL--PRAVLASPCVATVT ILDDDHAGIFTFECDTIHVSE 543
      | :  |  |  | | | |  | : : :  | :  :  |  | | |
Db      514 LQRL LGENISVRNLKLIMESIALWAPRE-----KD VITLVEHV RASLSRYICSKIAVSG 567

Qy      544 SIGVMEVKVLR TSG 557
      | : | :  | |
Db      568 -----EIKVVMLSG 576

```

RESULT 14

US-09-134-001C-3159

; Sequence 3159, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674

; SEQ ID NO 3159

; LENGTH: 10182

; TYPE: PRT

; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-3159

Query Match 3.0%; Score 97.5; DB 4; Length 10182;

Best Local Similarity 21.5%; Pred. No. 1e+02;

Matches 73; Conservative 56; Mismatches 133; Indels 77; Gaps 16;

```

Qy      310 DESRREMIRILKDLKQ---KHPEKD-----LDQLVEMANYYA-----LSHQQK 349
      | : ::: || | :| | :|| || |: ||::|
Db      9479 DATSNDLVNQAKDEGQSAIEHHADELPAKALDANQMIDQKVEDINHLISQNPNSNEEK 9538

Qy      350 SRAFYRIQATRMMTGAGN----ILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSY 405
      :: :| ::: | | : | | : : || : | :| :
Db      9539 NKLISQI--NKLVNGIKNEIQQAINKQIENA--TTKLDEVIETTKKLIIAKAE----AK 9590

Qy      406 QCLENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFS 465
      | :: : : | : | :|| || : || | |
Db      9591 QMIKELSQKKRDAINNNTDL-----TPSQKAHALADIDKTE-----KDALQHIENS 9636

Qy      466 VGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFN--SLPLPRAVLASPCVA---- 519
      | ||| || | |::: | : : | :| | | | :| |
Db      9637 NSI--DDINNKEHAFNTLAHIIIWDTDQQ----PLVFEVPELSLQNALVTSEVVHRDE 9690

Qy      520 -----TVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVE 570
      :| : | : :| |:: : :||| : | : || || : ||
Db      9691 TISLESIKKMTLTDELKVNIVSLP-NTDKVADHL-TAKVKVILADGSYVTNVVPVKVVE 9748

Qy      571 GTAKGGGEDFEDTYG-----ELEFKNDETVCDRQEA 601
      : :| | ::: | : | :::|
Db      9749 KELQIAKKDAIKTIDVLVKQKIKDIDSNNELTSTQREDA 9787

```

RESULT 15

US-09-107-532A-7193

; Sequence 7193, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

```

;      APPLICANT: Lynn A Doucette-Stamm  and David Bush
;      TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;                               ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND
THERAPEUTICS
;      NUMBER OF SEQUENCES: 7310
;      CORRESPONDENCE ADDRESS:
;          ADDRESSEE: GENOME THERAPEUTICS CORPORATION
;          STREET: 100 Beaver Street
;          CITY: Waltham
;          STATE: Massachusetts
;          COUNTRY: USA
;          ZIP: 02354
;      COMPUTER READABLE FORM:
;          MEDIUM TYPE: CD-ROM ISO9660
;          COMPUTER: PC
;          OPERATING SYSTEM: <Unknown>
;          SOFTWARE: ASCII
;      CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/107,532A
;          FILING DATE: 30-Jun-1998
;      PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 60/085,598
;          FILING DATE: 14 May 1998
;          APPLICATION NUMBER: 60/051571
;          FILING DATE: July 2, 1997
;      ATTORNEY/AGENT INFORMATION:
;          NAME: Ariniello, Pamela Deneke
;          REGISTRATION NUMBER: 40,489
;          REFERENCE/DOCKET NUMBER: GTC-012
;      TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (781)893-5007
;          TELEFAX: (781)893-8277
;      INFORMATION FOR SEQ ID NO: 7193:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 429 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          HYPOTHETICAL: YES
;          ORIGINAL SOURCE:
;              ORGANISM: Enterococcus faecium
;          FEATURE:
;              NAME/KEY: misc_feature
;              LOCATION: (B) LOCATION 1...429
;          SEQUENCE DESCRIPTION: SEQ ID NO: 7193:
US-09-107-532A-7193

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Query Match          3.0%;  Score 96.5;  DB 4;  Length 429;
Best Local Similarity 19.8%;  Pred. No. 0.61;
Matches   86;  Conservative   67;  Mismatches 158;  Indels 123;  Gaps   20;

```

```

Qy      107 SQEREVTIKKPNGETSTTTIRVW----NETVSNLTLMALGSSAPEILLSLIEVCGHGFIA 162
      | :: :   | | :   | : |   |   : : : : | : | : : |
Db      40  SNKQSIIVAVSPTG-SGKTLAYLWPLLLNVEPGEASALVIFASSQELAIQVADVAREWGKD 98

Qy      163 GDLGPSTIVGSAAFNMFIIGICVYVIPDGETRRIKHL-----RVFFITAAWSIFAYIWL 217
      : |   : : | |   |   |   : |   | : |   | :   : | | :

```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 24, 2004, 16:07:32 ; Search time 14.0818 Seconds
(without alignments)
4235.175 Million cell updates/sec

Title: US-10-054-680-4
Perfect score: 3228
Sequence: 1 MAWLRLQPLTSAFLHFGGLVT.....ADYGRRGGQEDSRDGKASIG 620

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2159.5	66.9	970	2	A36417	Na+/Ca2+-exchangin
2	2147.5	66.5	970	2	S27114	Na+/Ca2+-exchangin
3	2146.5	66.5	973	2	S32815	Na+/Ca2+-exchangin
4	2142.5	66.4	970	2	I48097	Na+/Ca2+-exchangin
5	2138	66.2	957	2	A53789	Na+/Ca2+-exchangin
6	2136.5	66.2	941	2	B53335	Na+/Ca2+-exchangin
7	2135.5	66.2	935	2	S43730	Na+/Ca2+-exchangin
8	2135.5	66.2	958	2	S32435	Na+/Ca2+-exchangin
9	2129.5	66.0	971	2	S28833	Na+/Ca2+-exchangin
10	1954.5	60.5	921	2	A54139	Na+/Ca2+-exchangin
11	1196.5	37.1	890	2	B89047	protein C10G8.5 [i
12	633.5	19.6	807	2	T24110	hypothetical prote
13	362.5	11.2	538	2	T00424	probable Na+/Ca2+

14	205	6.4	1014	2	T31433	Na+/Ca2+,K+-exchan
15	198.5	6.1	1199	2	S20969	Na+/Ca2+,K+-exchan
16	187	5.8	4936	2	AH2515	hypothetical prote
17	178.5	5.5	591	2	T19746	hypothetical prote
18	170	5.3	611	2	T21747	hypothetical prote
19	169.5	5.3	3016	2	S77300	hypothetical prote
20	166	5.1	1568	2	T08616	aggregation factor
21	156.5	4.8	2205	2	T08615	aggregation factor
22	150.5	4.7	591	2	S40705	Na+/Ca2+,K+-exchan
23	144.5	4.5	703	2	T03888	Na+/Ca2+,K+-exchan
24	144	4.5	644	2	B96582	hypothetical prote
25	144	4.5	1428	2	AC2224	hypothetical prote
26	132	4.1	1807	2	JC6319	integrin beta-4 ch
27	131.5	4.1	826	2	AB1841	hypothetical prote
28	131	4.1	590	2	S40707	hypothetical prote
29	126.5	3.9	1875	2	A36429	integrin beta-4 ch
30	126	3.9	4199	2	S76412	hypothetical prote
31	124	3.8	318	2	A83708	hypothetical prote
32	122	3.8	825	2	T08617	aggregation factor
33	121.5	3.8	651	2	T03889	Na+/Ca2+,K+-exchan
34	121.5	3.8	743	2	T38674	probable membrane
35	119.5	3.7	433	2	S74922	hypothetical prote
36	119	3.7	3972	2	S75251	hypothetical prote
37	115	3.6	324	2	AI0434	probable sodium/ca
38	114	3.5	1748	1	JN0786	integrin beta-4 ch
39	113	3.5	332	2	H82064	conserved hypothet
40	112.5	3.5	375	2	I40554	rap60 protein - Ba
41	110	3.4	2397	1	A55535	versican precursor
42	109	3.4	769	2	G95270	hypothetical prote
43	108.5	3.4	652	2	A37000	leukemia virus rec
44	108	3.3	673	1	VCPVB5	coat protein VP1 -
45	107.5	3.3	1263	2	T00649	hypothetical prote

ALIGNMENTS

RESULT 1

A36417

Na+/Ca2+-exchanging protein - dog

C;Species: Canis lupus familiaris (dog)

C;Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 18-Aug-2000

C;Accession: A36417

R;Nicoll, D.A.; Longoni, S.; Philipson, K.D.

Science 250, 562-565, 1990

A;Title: Molecular cloning and functional expression of the cardiac sarcolemmal Na(+)-Ca(2+) exchanger.

A;Reference number: A36417; MUID:91047958; PMID:1700476

A;Accession: A36417

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-970 <NIC>

A;Cross-references: GB:M57523; NID:g164072; PIDN:AAA62766.1; PID:g164073;

GB:M36119

C;Superfamily: human Na+/Ca2+-exchanging protein

C;Keywords: phosphoprotein; transmembrane protein

Query Match 66.9%; Score 2159.5; DB 2; Length 970;
 Best Local Similarity 69.9%; Pred. No. 2.8e-157;
 Matches 425; Conservative 73; Mismatches 89; Indels 21; Gaps 8;

```

Qy      1 MAWLRLQPLTSAFLHFGLVTFVLF--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
      | ||| | | | | | :|| :: : || | : || : ||| ||:||
Db      1 MLQLRLLPTFSMGCHLLAVVALLFSHVDLISAETEMEGERNETGE----CTGSYYCKKGV 56

Qy      59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN 118
      ||||| |::|| ||||| |||||::||| ||||| |||||::||| |||||
Db      57 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQKEITIKKPN 116

Qy     119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNM 178
      |||: ||:|:||||| ||||| |||||:||||| ||||| ||||| |||||
Db     117 GETTKTTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 176

Qy     179 FIIIGICVYVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL 238
      |||| :|||:||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     177 FIIIALCVYVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF 236

Qy     239 FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH 295
      ||||:|:| ||||:||||| ||||:|:| ||| ||| |||||:|:|
Db     237 FFFPICVVFVAVADRLLLFYKYVYKRYRAGKQRMIIIEHGEDRPSSKTEIEMDGKVVNSH 296

Qy     296 ---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 348
      |||| || || | | | :||| ||||:||||| ||||:|:| ||| |||
Db     297 VDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355

Qy     349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
      ||||| |||||:||||| ||||:|:| || |||:| | | :||:|:| :|||
Db     356 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTYQC 415

Qy     408 LENC GAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGT VVLKPGETQKEFSVG 467
      ||||| | ||::|:|:|:| :||:|:| ||||:||||| ||||| |||
Db     416 LENC GTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGT VVFKPGETQKEIRVG 475

Qy     468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPAIFNSLPLPRAVLASPCVATVTILDDD 527
      ||||| ||||:| | ||||:| | |:| | | | | |||| |||
Db     476 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---ALACLGSPSTATVTIFDDD 532

Qy     528 HAGIFTFECDTIHVSESIGVMEVKVLRRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
      ||||| |||||:||||| ||||:|:| ||||:|:| ||||| |||
Db     533 HAGIFTFEEPVTHVSESIGIMEVKVLRRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy     588 EFKNDETV 595
      ||:| | |
Db     593 EFQNDEIV 600

```

RESULT 2

S27114

Na⁺/Ca²⁺-exchanging protein precursor, cardiac - bovine

N;Alternate names: Na⁺/Ca²⁺ antiporter

C;Species: Bos primigenius taurus (cattle)

C;Date: 22-Nov-1993 #sequence_revision 23-Mar-1995 #text_change 18-Aug-2000

C;Accession: S27114; S18388

R;Aceto, J.F.; Condrescu, M.; Kroupis, C.; Nelson, H.; Nelson, N.; Nicoll, D.; Philipson, K.D.; Reeves, J.P.
Arch. Biochem. Biophys. 298, 553-560, 1992
A;Title: Cloning and expression of the bovine cardiac sodium-calcium exchanger.
A;Reference number: S27114; MUID:93037494; PMID:1416984
A;Accession: S27114
A;Molecule type: mRNA
A;Residues: 1-970 <ACE>
A;Cross-references: GB:L06438; NID:g163033; PIDN:AAA30509.1; PID:g163034
R;Durkin, J.T.; Ahrens, D.C.; Pan, Y.C.E.; Reeves, J.P.
Arch. Biochem. Biophys. 290, 369-375, 1991
A;Title: Purification and amino-terminal sequence of the bovine cardiac sodium-calcium exchanger: evidence for the presence of a signal sequence.
A;Reference number: S18388; MUID:92027750; PMID:1929404
A;Accession: S18388
A;Molecule type: protein
A;Residues: 33-40,'X',42-44 <DUR>
A;Experimental source: heart
C;Superfamily: human Na⁺/Ca²⁺-exchanging protein
C;Keywords: cardiac muscle; heart; ion transport; membrane protein
F;1-32/Domain: signal sequence #status predicted <SIG>
F;33-970/Product: Na⁺/Ca²⁺ exchange protein, cardiac #status predicted <MAT>

Query Match 66.5%; Score 2147.5; DB 2; Length 970;
Best Local Similarity 69.4%; Pred. No. 2.4e-156;
Matches 422; Conservative 74; Mismatches 91; Indels 21; Gaps 8;

Qy	1	MAWLRLQPLTSAFLHFGVLTVFLV--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV	58
		: : : : : :	
Db	1	MLQFSLSPTLSMGFHVIAVALLFSHVDHISAETEMEGEGNETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN	118
		: : : : :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNM	178
		: : : :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM	176
Qy	179	FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLMLAVFSPGVVQWEGLLTL	238
		: : : : : : :	
Db	177	FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH	295
		: : : : : : :	
Db	237	FFFPICVFAWVADRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPSSKTEIEMDGKVVNSH	296
Qy	296	---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLQLVEMANYALSHQQ	348
		: : : : :	
Db	297	VDSFLDGALV-LEVDERDQDDEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355
Qy	349	KSRIFYRIQATRMMTGAGNILLKHAEEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC	407
		: : : : : : : : :	
Db	356	KSRIFYRIQATRLMTGAGNILLKHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTYYQC	415
Qy	408	LENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
		: : : : : : : : : : : : : : :	

Db	416	L E N C G T V A L T I I R R G G D L T N T V F V D F R T E D G T A N A G S D Y E F T E G T V V F K P G E T Q K E I R V G	475
Qy	468	I I D D D I F E E D E H F F V R L S N V R I E E E Q P E E G M P P A I F N S L P L P R A V L A S P C V A T V T I L D D D : : : : :	527
Db	476	I I D D D I F E E D E N F L V H L S N V K V S L E A S E D G I L E A S H V S - - T L A C L G S P S T A T V T I F D D D	532
Qy	528	H A G I F T F E C D T I H V S E S I G V M E V K V L R T S G A R G T V I V P F R T V E G T A K G G G E D F E D T Y G E L : : : : : :	587
Db	533	H A G I F T F E E P V T H V S E S I G I M E V K V L R T S G A R G N V I V P Y K T I E G T A R G G G E D F E D T C G E L	592
Qy	588	E F K N D E T V	595
Db	593	E F O N D E I V	600

Query Match 66.5%; Score 2146.5; DB 2; Length 973;
Best Local Similarity 69.2%; Pred. No. 2.8e-156;
Matches 421; Conservative 76; Mismatches 90; Indels 21; Gaps 8;

Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHFIAGDLGPSTIVGSAAFNM	178
Db	120	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM	179
Qy	179	FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL	238
Db	180	FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF	239
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKHGGIIETEGDHPKG---IEMDGKMMNSH	295
Db	240	FFFPICVVFVAVVADRRLLFYKYVYKRYRAGKQGRGMIIEHEGDRPSSKTEIEMDGKVVNSH	299
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQLVEMANYYALSHQQ	348
Db	300	VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLSQQQ	358
Qy	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC	407
Db	359	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVTENDPVSKIFFEQGTYYQC	418
Qy	408	LENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
Db	419	LENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGDTQKEIRVG	478
Qy	468	IIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPAIFNSLPLPRAVLASPCVATVTILDDD	527
Db	479	IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD	535
Qy	528	HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTEGTAKGGGEDFEDTYGEL	587
Db	536	HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL	595
Qy	588	EFKNDETV	595
Db	596	EFONDEIV	603

Query Match 66.4%; Score 2142.5; DB 2; Length 970;
Best Local Similarity 69.1%; Pred. No. 5.7e-156;

Matches 420; Conservative 76; Mismatches 91; Indels 21; Gaps 9;

```

Qy      1 MAWLRLQPLTSAFLH-FGLVTFVL-FLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MLRLSLSPYSLGFLHLLAMMTLLISHVDHITAET----EMVEEGNETGECTGSYYCKKGV 56

Qy     59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN 118
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     57 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPN 116

Qy    119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAAFNM 178
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    117 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAAFNM 176

Qy    179 FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL 238
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    177 FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF 236

Qy    239 FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHGGIIETEGDHPKG---IEMDGKMMNSH 295
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    237 FFFPICVFAVADRRLLFYKYVYKRYRAGKQRMIIIEHEDRPSSKTEIEMDGKVVNSH 296

Qy    296 ---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYALSHQQ 348
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    297 VENFLDGALV-LEVDERDQDDEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355

Qy    349 KSRAFYRIQATRMGTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    356 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTVAENDPVSKIFFEQGTQYC 415

Qy    408 LENCNAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    416 LENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKEPGETQKEIRVG 475

Qy    468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPAIFNSLPLPRAVLASPCVATVTILDDD 527
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    476 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHIS---TLACLGSPSTATVTIFDDD 532

Qy    528 HAGIFTFECDTIHVSESIGVMEVKVLRRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    533 HAGIFTFEEPVTHVSESIGIMEVKVLRRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy    588 EFKNDETV 595
      | | | | |
Db    593 EFQNDIV 600

```

RESULT 5

A53789

Na⁺/Ca²⁺-exchanging protein precursor, splice form NACA7 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 18-Aug-2000

C;Accession: A53789; JX0288

R;Lee, S.L.; Yu, A.S.L.; Lytton, J.

J. Biol. Chem. 269, 14849-14852, 1994

A;Title: Tissue-specific expression of Na⁽⁺⁾-Ca⁽²⁺⁾ exchanger isoforms.

A;Reference number: A53789; MUID:94253030; PMID:8195112

A;Accession: A53789
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-957 <LEE>
 A;Cross-references: GB:U04933; NID:g451571; PIDN:AAB39952.1; PID:g451572
 R;Nakasaki, Y.; Iwamoto, T.; Hanada, H.; Imagawa, T.; Shigekawa, M.
 J. Biochem. 114, 528-534, 1993
 A;Title: Cloning of the rat aortic smooth muscle Na⁺/Ca²⁺ exchanger and tissue-specific expression of isoforms.
 A;Reference number: JX0288; MUID:94103175; PMID:8276763
 A;Accession: JX0288
 A;Molecule type: mRNA
 A;Residues: 1-957 <NAK>
 A;Experimental source: aortic smooth muscle
 C;Superfamily: human Na⁺/Ca²⁺-exchanging protein
 C;Keywords: ion transport; membrane protein
 F;1-32/Domain: signal sequence #status predicted <SIG>
 F;33-957/Product: Na⁺/Ca²⁺ exchanger #status predicted <MAT>

Query Match 66.2%; Score 2138; DB 2; Length 957;
 Best Local Similarity 67.9%; Pred. No. 1.2e-155;
 Matches 424; Conservative 73; Mismatches 87; Indels 40; Gaps 10;

Qy	4	LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK	55
		: : : :	
Db	2	LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK	53
Qy	56	EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK	115
		: :: :: : : : :	
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK	113
Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAA	175
		: : :	
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL	235
		: : :	
Db	174	FNMFIIALCVYVVPDGETRGIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGL	233
Qy	236	LTLFFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIETEGDHPKG---IEMDGKMM	292
		: : : : : : :	
Db	234	LTFPPFPICVFAWVADRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPASKTEIEMDGKVV	293
Qy	293	NSH---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYALS	345
		: : : : : : :	
Db	294	NSHVDNFLDGLV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qy	346	HQQKSRAFYRIQATRMGTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
		: : : : : : : : : :	
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKEVFEQGT	412
Qy	405	YQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
		: : : : : : : : : : : : : : : :	
Db	413	YQCLENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qy	465	SVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
		: : : : : :	


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Db          473 RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528
Qy          524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
            |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db          529 FDDDHAGIFTFEPEVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588
Qy          584 YGELEFKNDETV-----CDRQE 600
            ||||:|||| | ||:|
Db          589 CGELEFQNDIVKIITIRIFDREE 612

```

RESULT 6

B53335

Na+/Ca2+-exchanging protein NCX1, splice form NACA6 - rabbit

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 18-Aug-2000

C;Accession: B53335

R;Kofuji, P.; Lederer, W.J.; Schulze, D.H.

J. Biol. Chem. 269, 5145-5149, 1994

A;Title: Mutually exclusive and cassette exons underlie alternatively spliced isoforms of the Na/Ca exchanger.

A;Reference number: A53335; MUID:94148976; PMID:8106495

A;Accession: B53335

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-941 <KOF>

A;Experimental source: brain

A;Note: sequence extracted from NCBI backbone (NCBIP:144050)

C;Superfamily: human Na+/Ca2+-exchanging protein

```

Query Match          66.2%; Score 2136.5; DB 2; Length 941;
Best Local Similarity 69.5%; Pred. No. 1.6e-155;
Matches 417; Conservative 76; Mismatches 86; Indels 21; Gaps 9;

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```

Qy          8 PLTSAFLHFGVLVTFVLF-LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPE 66
            | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db          9 PFSMGFHLIAIVALFFFRVDHVSASETMEGEGNETGE-----CTGSYYCKKGVLPIWEPQ 64

Qy          67 NPSLGDKIARVIVYFVALIYMFLGVSIADRFRMASIEVITSQEREVTIKKPNGETSTTTI 126
            :|| ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||:
Db          65 DPSFGDKIARATVYFVAMVYMFLGVSIADRFRMSSIEVITSQEKEITIKK-NGETTKTTV 123

Qy          127 RVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAAFNMFIIIGICV 186
            |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||:
Db          124 RIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIIALCV 183

Qy          187 YVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFFFPVCVL 246
            ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: ||:
Db          184 YVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGIVEVWEGLLTFFFFPICVV 243

Qy          247 LAWVADKRLLFYKYMHHKRYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH---FLDGN 300
            |||||:|||||:||||| | ||: || | | |||||:|||| | |||
Db          244 FAWVADRRLLFYKYVYKRYRAGKQRMIIIEHGEDRPSSKTEIEMDGKVNSHVDNFDGA 303

Qy          301 LVPLEGKEVD-----ESRREMIRILKDLKQKHPEKDLQVEMANYALSHQQKSRAFYRI 356
            || | : | | | : |||| ||||:|||||:|||||:|||||: || |||||
Db          304 LV-LDVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQKSRAFYRI 362

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Qy	4	LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK	55
		: : :	
Db	2	LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK	53
Qy	56	EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK	115
		: : : : : : : : :	
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIK	113
Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA	175
		: : : :	
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAA	173
Qy	176	FNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEG	235
		: : : : : :	
Db	174	FNMFIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSPGVVEVWEG	233
Qy	236	LTLFFFPVCVLLAWVADKRLLEFYKYMHHKYRTDKHRGIIIIETEGDHPKG---IEMDGKMM	292

[illegible]

A54139

Query Match 60.5%; Score 1954.5; DB 2; Length 921;
Best Local Similarity 64.1%; Pred. No. 1.4e-141;
Matches 371; Conservative 92; Mismatches 91; Indels 25; Gaps 6;

Qy	31	EAGGSGDVPSTGQNNE-----SCSGSSDCKEGVILPIWYPENPSLGDK IARVIVYFVALI	85
Db	21	EATPTPSLPPPPANDSDASPGGCQGSYRCQPGVLLPVWEPDDPSLGDKAARAVVYFVAMV	80
Qy	86	YMFLGVSI IADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSA	145
Db	81	YMFLGLSIIADRFMASIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSA	140
Qy	146	PEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI IIGICVYVIPDGETR KIKHLRVFFI	205
Db	141	PEILLSVIEVCGHNFQAGELGPGTIVGSAAFNMFVVI AVCVYVIPAGESR KIKHLRVFFV	200
Qy	206	TAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFF PVCVLLAWVADKRL LFYKYMHKKY	265
Db	201	TASWSIFAYVWLYLILAVFSPGVVQVWEALLTLVFF PFCVVF FAWMADKRL LFYKYVYKRY	260
Qy	266	RTDKHRGII IETEGDHPKGIEMDGKMMNSHFLDGNL-----VPLEGKEVDESRRMIRIL	320
Db	261	RTDPRSGII IGAEGDPPKSIELDGTFVGTE-VPGELGALGTGPAEARELDASRREVIQIL	319
Qy	321	KDLKQKHPEKDL DQLVEMANYYALSHQ QKSRAF YRIQATRM MTGAGN I LKKHAAEQAKKA	380
Db	320	KDLKQKHPPDKDLEQLVGI AKYYALLHQ QKSRAF YRIQATRL MTGAGN VLR RHAADAARRP	379
Qy	381	SSMSEVHTDEPEDFISKVFFDPCS YQCLENC GAVLLTVVRKGGDMSK TMYVDYKTEDGSA	440
Db	380	GA-NDGAPDDEDDGASRIFFEPSLYHCL ENCGSVLLSVACQGGEGNSTFYVDYRTEDGSA	438
Qy	441	NAGADYEFTEGT VVLKPGETQKEFSVGIIDDDI FEEDEHFFVRLSNVRIEEEQ-----PEE	496
Db	439	KAGSDY EYSEGTLVFKPGETQKELRIGIIDDDI FEEDEHFFVRLNL RVGDAQGMFEPDG	498
Qy	497	GMPPAIFNSLPLPRAVLASPCVATVTILDDD HAGIFTFECDTIHVSESIGVMEVKVLR TS	556

```

Db          |          | : | : | : ||||| ||||| : : | : | : | : | : |
499 G-----GRPKGRLVAPLLATVTILDDDHAGIFS FQDRLLHVSECMGTVDVRVVRSS 549

QY          557 GARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
          ||||| : | : | : ||| : || ||||| : ||| :
Db          550 GARGTVRLPYRTVDGTARGGGVHYEDACGELEFGDDETM 588

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RESULT 11

B89047

protein C10G8.5 [imported] - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text change 24-May-2001

C;Accession: B89047

R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998

A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology.

A;Reference number: A75000; MUID:99069613; PMID:9851916

A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/ for a list of authors

A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 285, 1493, 1999

A;Accession: B89047

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-890 <STO>

A;Cross-references: GB:chr_V; PIDN:AAB09172.1; PID:g1572830; GSPDB:GN00023;
CESP:C10G8.5

C;Genetics:

A;Gene: C10G8.5

```
A;Map position: 5
```

C;Superfamily: human Na⁺/Ca²⁺-exchanging protein

Query Match 37.1%; Score 1196.5; DB 2; Length 890;

Best Local Similarity 47.6%; Pred. No. 1.9e-83;

Matches 243; Conservative 97; Mismatches 150; Indels 21; Gaps 7;

QY 87 MFLGVSIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAP 146
 |||::|:||||:||||| || : ::| : :|::|:|||||
 Db 1 MFLGISIVADRFMSSIEVITSMERTIVVKRPLDPMVQVRIWNDTVSNLTLMALGSSAP 60

QY 147 EILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRGIKHLRVFFIT 206
 ||||:| | |||||:|||||||:|:| | | | | : | | | : |
 Db 61 EILLSIIEVIARGFEAGDLGPNTIVGSAAFNLFMIIAICVWVWIPKGEIRROKHLDVFCVT 120

QY 207 AAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYR 266
| ||: ||: ||: ||: || ||| :: || || |||: | |: || |: | :: : ||
Db 121 ATWSVFAYVWLYLILAFFSPGEIEIWEGALTFIFFPLTVFTAYMADIKLIONKFLPHRYR 180

Qy 267 TDKHRGIIIE TEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQK 326
| | : | | : | : | : | | : | | : | : | : | :
Db 181 RGS H-GQM IATEAEEMKM L E-----NGT QGD PALKAFEEHROEFIELMREIRKO 228

Qy 327 HPEKDL DQLVEMANY YALSHQQKS RAFYRI QATRM MTGAGN ILKKHAAEQAKKA-SSMSE 385
 :| :| : | | :| ||||| |:|||| : | |:|:| :: || :::
Db 229 NPHITP TELQ KQA EYEMI SRGP KSRAFY RVQATR RLIGGG DIVKKRID KEHNKALDALVO 288

Db 55 SATKKVKKQKKAGQLVAKEEDEEIDEQYDYVRIWNPTVANLTLMALGSSAPEILLSIIEI 114
 Qy 156 CGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKHKLRLVFFITAAWSIFAYI 215
 |::| ||||| |||||::| | ||: : :|::|: ||: |::|
 Db 115 VGNGFKAGDLGPGTIVGSAAFNLFCSAICVFAV-GTQTKRIELYRVFVTAFFGT FayI 173
 Qy 216 WLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTD----- 268
 |:::| | :| || ||| :||| || : |::: | :: | | :|
 Db 174 WVFLVLIVITPNVVDVWEAILTLFFIILVVVSYAVDAQI----WKKKKSSDLQEELEM 228
 Qy 269 -KHRGIIIEGTEGHPKGIEMDGKMMNSHFL----DGNLVPLEGKEVDESRR----- 314
 :| | : | | : : | | : : : : | | |
 Db 229 AQHDGKV---DDQPEKLSDEIKKWASNLSLNKEENDVIVDATPSVDTVRRWTRTSISHTY 284
 Qy 315 -----EMIRILKDLKQKHPEKDLDQLVEMANYYYALSHQQ 348
 | | : | : : : : | | :
 Db 285 PSLSDEDQAKILAYRVSRMTSHDRLYRIRAIRQLSSSWRKSEEEVLKMNQESTDSAS 344
 Qy 349 KSRAF-----YRIQAT-----RMTGAGNILKKHAAEQAK-----KASSM 383
 : : | | : | : : : | | : | : : | : :
 Db 345 RRKTFVEFSARVYRVDATDET VSLKIERKGNMESKFTVSYATVNGLAKKDLNFLFKSETL 404
 Qy 384 ----SEVH-----TDEPEDFISKVFFDPC--SYQCLENCG 412
 | : | | | | | | : | : | | |
 Db 405 QFNPGELHKTISIQLINAANWRPNDFYVHLKIQDVDED--SKICLGACNVAVVVKENAG 462
 Qy 413 AVLLTVVRKGGMSKTMVVDYKTEDGSANAGADY-EFTEGTVVLKPGETQKEFSVGIIDD 471
 | | : | : | | : | | : | : : | : | : : | |
 Db 463 FRSFVTRRGGLKKPLQVHYETEDVTAKQGDDYTAVKDGILGFEGQEYKYIDIDVIDD 522
 Qy 472 DIFEDEHFFVRLSNVRIEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDH 528
 : | : | | : | : : : | : : | : | : | :
 Db 523 KMDEKDEAFIIEI--LKVDE-----PGVSIGTRRKATITIISDDN 560

RESULT 13

T00424

probable Na⁺/Ca²⁺ antiporter [imported] - Arabidopsis thaliana

N;Alternate names: hypothetical protein T30B22.10

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001

C;Accession: T00424; C84917

R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Mason, T.M.; Kerlavage, A.R.; Adams, M.D.; Somerville, C.R.; Venter, J.C. submitted to the EMBL Data Library, October 1998

A;Description: Arabidopsis thaliana chromosome II BAC T30B22 genomic sequence.

A;Reference number: Z14149

A;Accession: T00424

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-538 <ROU>

A;Cross-references: EMBL:AC002535; NID:g2529657; PID:g3522931

A;Experimental source: cultivar Columbia

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams,

M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: C84917

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-538 <STO>

A;Cross-references: GB:AE002093; NID:g3522931; PIDN:AAC62871.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g47600; T30B22.10

A;Map position: 2

A;Introns: 131/1; 189/3; 229/2; 287/1; 333/1; 397/1; 440/2

Query Match 11.2%; Score 362.5; DB 2; Length 538;
Best Local Similarity 31.3%; Pred. No. 9.3e-20;
Matches 91; Conservative 61; Mismatches 96; Indels 43; Gaps 9;

```
QY      64 YPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETST 123
      :|  :|  | : | ::||: | | |:|:| | || |:| :   |:|   | :
Db      29 FPGENTLSDGL-RGVLYFLGLAYCFIGLSAITARFFKSMENVVKHSRKVVTIDPITKAEV 87

QY      124 TTI-RVWNETVSNLTLMALGSSAPEILLSLIEV---CGHGFIAGDLGPSTIVGSAAFNMF 179
      | :||| |:::|:| | :| | :| | : |   | : || ||| |:|||||::|
Db      88 ITYKKVWNFTIADISLLAFGTSFPQISLATIDAIRNMGERY-AGGLPGTTLVGSAAFDLF 146

QY      180 IIIGICVYVIPDGETRIKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLF 239
      | :|| |   || :|| | | : :   || :|||||:| | |:| | : : | |||:
Db      147 PIHAVCVVVPKAGELKKISDLGVWLVELVWSFWAYIWLYIILEVWSPNVITLVEALLTVL 206

QY      240 FFPVCVLLAWVADKRLLFYKYMHHKRYRTDKHRGIIIEGTDHPKGIEMDGKMMNSHFLDG 299
      : : : : |: ||| : |:   : : || |:
Db      207 QYGLLLVHAYAQDKR---WPYLS-----LPMSRGDRPE----- 236

QY      300 NLVPLEGKEVDESR----REMIRILKDLKQKHPEKDLQVLVEMANYYALSH 346
      ||  :|:| |:   : : | | |   :|: : : : :
Db      237 EWVP---EEIDTSKDDNDNDVHDVYSDAQAQDAVESGSRNIVDIFSISANN 284
```

RESULT 14

T31433

Na⁺/Ca²⁺,K⁺-exchanging protein - bottle-nosed dolphin

C;Species: *Tursiops truncatus* (bottle-nosed dolphin)

C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C;Accession: T31433

R;Cooper, C.B.; Winkfein, R.J.; Schnetkamp, P.P.M.

submitted to the EMBL Data Library, April 1998

A;Description: Cloning, sequencing, and functional expression of the bottlenose dolphin retinal rod Na/Ca+K exchanger reveals a cytosolic inhibitory domain.

A;Reference number: Z21032

A;Accession: T31433

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-1014 <COO>

A;Cross-references: EMBL:AF059031; NID:g3170602; PID:g3170603; PIDN:AAC18119.1
C;Genetics:
A;Gene: NCKXr

Query Match 6.4%; Score 205; DB 2; Length 1014;
Best Local Similarity 23.6%; Pred. No. 2.7e-07;
Matches 105; Conservative 65; Mismatches 161; Indels 114; Gaps 19;

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Qy      77 VIVYFVALIYMFLGVSIIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN 135
      |:::  ::||: ::||: | |::: ||| :          ::: || |:
Db      451 VVLHIFGMLYVFVALAIVCDEYFVPALGVITDK-----LQI-SEDVAG 492

Qy      136 LTLMALGSSAPEILLSLIEVCGHGFIA-GDLGPSTIVGSAAFNMFIIIGICVYVIPDGET 194
      | || | ||||: ||| :   ||: ::| ||||| ||: :|| |   :
Db      493 ATFMAAGGSAPLEFTSLIGI----FISHSNVGIGTIVGSAVFNILFVIGTCALF-----S 543

Qy      195 RKIKHLRVFFITAAWSIFAYIWLY-----MILAVFSPGVVQVWEGLLTLFFFPVCVL-LA 248
      |:| :|      | :| | |      |:: |   :: |||| | : : | :
Db      544 REILNL-----TWWPLFRDITFYILDMLLILFFFLDSLIVWWESLLLLLAYALYVFTMK 597

Qy      249 WVADKRLLFYKYMHHK-----YRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGNLV 302
      |      | | : ::      | : | : | |      | | : :
Db      598 WNKQLELWVKQLSRRPVPKVMALGDLSKGDVAEAS---TGERTDNEVK-----T 645

Qy      303 PLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQQK--SRAFYRIQATR 360
      | ||: ::| |      || : :: | : : : :| : : ||| |
Db      646 PGEGENGEQSGGE-----AQPEGEKEEGKGENESEGDIQAERKGENESEGDIQAER 695

Qy      361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      |      | :|      | : || :      |      |
Db      696 KGDDEG-----EGEIQAGEDGEMKGDEGD-----LQAER 724

Qy      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGI-----IDD 471
      || | :      ||| | | | | : : : || | |      :
Db      725 KGDDEGEGEI--QAGEDGEMK-GDDGETGEQDLIADNQDDAKEDEKGIDGEEEGDGGGESE 781

Qy      472 DIFEEDEHFFVRLSNVRIEEEQPEE 496
      | ||:|      |||| ||
Db      782 DEEEEEEEGEEEEEQEEEEEQEEE 806
```

RESULT 15

S20969

Na⁺/Ca²⁺,K⁺-exchanging protein - bovine

N;Alternate names: Na⁺/Ca²⁺,K⁺ antiporter; Na/Ca,K-exchanger

C;Species: Bos primigenius taurus (cattle)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C;Accession: S20969

R;Reilaender, H.; Achilles, A.; Friedel, U.; Maul, G.; Lottspeich, F.; Cook, N.J.

EMBO J. 11, 1689-1695, 1992

A;Title: Primary structure and functional expression of the Na/Ca,K-exchanger from bovine rod photoreceptors.

A;Reference number: S20969; MUID:92258377; PMID:1582405

A;Accession: S20969

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1199 <REI>

A;Cross-references: GB:X66481; NID:g505578; PIDN:CAA47108.1; PID:g505579

Query Match 6.1%; Score 198.5; DB 2; Length 1199;
Best Local Similarity 21.7%; Pred. No. 1.1e-06;
Matches 132; Conservative 74; Mismatches 210; Indels 193; Gaps 27;

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Qy      77 VIVYFVALIYMFLGVSIIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN 135
      |:::  ::|::|: ::|: | |:: :: ||| :          ::: :| |:
Db      449 VVLHIFGMMYVFVALAIVCDEYFVPALGVITDK-----LQI-SEDVAG 490

Qy      136 LTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGET 194
      | || | |||: ||| | ||: ::| ||||| ||: :|| | :
Db      491 ATFMAAGGSAPELFTSLIGV----FISHSNVGIGTIVGSAVFNILFVIGTCALF-----S 541

Qy      195 RKIKHLRVFFITAAWSIFAYIWLY----MILAVFSPGVVQVWEGLLTLFFFPVCVL-LA 248
      |:| :| | :| | | | |:: | :: || :| | : | :
Db      542 REILNL-----TWWPLFRDITFYIFDLMLLILFFLDSLIAWWESVLLLLLAYAFYVFTMK 595

Qy      249 WVADKRLLFYKYMHHK-----YRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDG 299
      | | : ::| : : | : | : | : | : :
Db      596 WNQQLWVKEQLNKRPAKVMALGDLSPKPGDGTVVVDEQQDNKKLKLSSMLTRG----S 651

Qy      300 NLVPLEGKEVDESRE-MIRILKDLKQKHPEKDLQ--LVEMANYALSHQQKSRIFYRI 356
      : | : : : |: | | : | || :: |: |
Db      652 SSASLHNSTIRSTIYQLMLHSLDPLGEARPSKDKEETLIPEAK----- 695

Qy      357 QATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-----DFISKVFFDPCSYQC 407
      | || | | | | | | | | |
Db      696 -----ATPQAKAESKPEEPAKLPEVTVTPAPAPDVKGDQEEDPGSQGV 739

Qy      408 ---LENCG-----AVLLTVVRKGGDMSKTMVVDYKTEDGS-----ANAGADYEFT 449
      || | | | | | | | | : : | | : | | |
Db      740 GAEAENTGERTGGEAEAPAEGENERSGGDAALGGESEGKAENESEGDIPAERRGDDE-D 798

Qy      450 EGTVVLKPGETQKEFSVGII-----DDDIFF-----EDEHFFVRLSNV 487
      || : : || : : | | | : | | | | :
Db      799 EGEIQAEGGEVKGDEDEGEIQAGEGGEVEGDEDEGEIQAGEGGEVEGDEDE-----GEI 852

Qy      488 RIEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGV 547
      : | || | : | | | | | : | | |
Db      853 QAGEAGEVEG-----DEDEGEIQAGEAGEVEGDEDEGE 885

Qy      548 MEVKVLRTSGARGTVIVPFRTVEGTAKGG-----GEDFEDTYGELEFKNDETVCDRQEA 601
      :: :| | | : || : | || | | :| | |
Db      886 IQ-----AGEGGEV----KGDEGEIQAGEAGEVEGED-----GEVEGGEDEGEIQAGEG 930

Qy      602 DYGRGGQE 610
      | | ||
Db      931 GEGETGEQE 939
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Search completed: June 24, 2004, 16:15:03
Job time : 16.0818 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 24, 2004, 16:12:03 ; Search time 34.1986 Seconds
(without alignments)
5118.180 Million cell updates/sec

Title: US-10-054-680-4
Perfect score: 3228
Sequence: 1 MAWLRLQPLTSAFLHFGGLVT.....ADYGRRGGQEDSRDGKASIG 620

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Match	Length	DB	ID	Description
No.						

1	3228	100.0	620	13	US-10-054-680-4	Sequence 4, Appli
2	3093	95.8	595	14	US-10-256-537-2	Sequence 2, Appli
3	3093	95.8	921	9	US-09-804-474A-2	Sequence 2, Appli
4	3093	95.8	921	13	US-10-054-680-2	Sequence 2, Appli
5	3093	95.8	925	14	US-10-114-153-4	Sequence 4, Appli
6	3093	95.8	927	14	US-10-275-116-2	Sequence 2, Appli
7	3093	95.8	928	14	US-10-114-153-2	Sequence 2, Appli
8	3016	93.4	927	9	US-09-804-474A-4	Sequence 4, Appli
9	2940	91.1	895	14	US-10-114-153-6	Sequence 6, Appli
10	2147.5	66.5	970	9	US-09-901-419-2	Sequence 2, Appli
11	2143.5	66.4	609	9	US-09-864-761-33429	Sequence 33429, A
12	1961	60.7	921	14	US-10-281-866-2	Sequence 2, Appli
13	1196.5	37.1	890	15	US-10-369-493-6319	Sequence 6319, Ap
14	633.5	19.6	807	15	US-10-369-493-6148	Sequence 6148, Ap
15	633.5	19.6	807	15	US-10-369-493-6149	Sequence 6149, Ap
16	243	7.5	161	12	US-10-424-599-228842	Sequence 228842,
17	203.5	6.3	106	14	US-10-256-537-5	Sequence 5, Appli
18	203.5	6.3	661	13	US-10-094-214-5	Sequence 5, Appli
19	203.5	6.3	661	14	US-10-281-868-2	Sequence 2, Appli
20	203.5	6.3	661	15	US-10-391-399-17	Sequence 17, Appl
21	202	6.3	6304	14	US-10-147-026-16	Sequence 16, Appl
22	197	6.1	546	12	US-10-276-774-2632	Sequence 2632, Ap
23	194.5	6.0	500	14	US-10-264-104-2	Sequence 2, Appli
24	186.5	5.8	644	15	US-10-353-690-18	Sequence 18, Appl
25	184	5.7	2092	14	US-10-147-026-12	Sequence 12, Appl
26	180.5	5.6	603	9	US-09-961-679-2	Sequence 2, Appli
27	178.5	5.5	591	15	US-10-369-493-6463	Sequence 6463, Ap
28	178.5	5.5	591	15	US-10-369-493-6464	Sequence 6464, Ap
29	175	5.4	1081	16	US-10-408-765A-298	Sequence 298, App
30	171.5	5.3	2780	12	US-10-423-483-2	Sequence 2, Appli
31	171.5	5.3	2780	15	US-10-220-587-2	Sequence 2, Appli
32	170	5.3	611	15	US-10-369-493-5204	Sequence 5204, Ap
33	162.5	5.0	1577	14	US-10-219-834-150	Sequence 150, App
34	161	5.0	759	15	US-10-415-378-15	Sequence 15, Appl
35	161	5.0	2753	12	US-10-262-511-160	Sequence 160, App
36	161	5.0	2753	12	US-10-262-511-166	Sequence 166, App
37	161	5.0	3838	12	US-10-262-511-162	Sequence 162, App
38	158.5	4.9	1615	14	US-10-219-834-149	Sequence 149, App
39	154	4.8	2777	12	US-10-423-483-4	Sequence 4, Appli
40	154	4.8	2777	15	US-10-220-587-4	Sequence 4, Appli
41	146	4.5	35	12	US-10-423-483-24	Sequence 24, Appl
42	146	4.5	35	15	US-10-220-587-24	Sequence 24, Appl
43	136.5	4.2	461	15	US-10-104-047-2842	Sequence 2842, Ap
44	135.5	4.2	1469	12	US-10-262-511-164	Sequence 164, App
45	133.5	4.1	227	14	US-10-264-104-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
 US-10-054-680-4
 ; Sequence 4, Application US/10054680
 ; Publication No. US20020132998A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Friddle, Carl Johan

```
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998A1el Human Ion Exchanger Proteins and
Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 620
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-054-680-4
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Query Match          100.0%; Score 3228; DB 13; Length 620;
Best Local Similarity 100.0%; Pred. No. 5.7e-315;
Matches 620; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120

Qy     121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180

Qy     181 IIGICVYVIPDGETRKKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 IIGICVYVIPDGETRKKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240

Qy     241 FPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 FPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300

Qy     301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR 360

Qy     361 MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCS YQCLENCGAVLLTVVR 420
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCS YQCLENCGAVLLTVVR 420

Qy     421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGT VVLKPGETQKEFSVGIIDDDIFEDEHF 480
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 KGGDMSKTMYVDYKTEDGSANAGADYEFTEGT VVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy     481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
```

```

Qy      541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVCDRQE 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETVCDRQE 600

Qy      601 ADYGRRGGQEDSRDGKASIG 620
          ||||||||||||||||
Db      601 ADYGRRGGQEDSRDGKASIG 620

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RESULT 2

US-10-256-537-2

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; Sequence 2, Application US/10256537
; Publication No. US20030162196A1
; GENERAL INFORMATION:
; APPLICANT: Carroll, Joseph M.
; TITLE OF INVENTION: METHODS OF USING 69039, A NOVEL HUMAN
; TITLE OF INVENTION: NA/CA EXCHANGER FAMILY MEMBER
; FILE REFERENCE: MPI01-231PlRM
; CURRENT APPLICATION NUMBER: US/10/256,537
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/325,737
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-256-537-2

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Query Match          95.8%; Score 3093; DB 14; Length 595;
Best Local Similarity 100.0%; Pred. No. 2e-301;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120

Qy      121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180

Qy      181 IIGICVYVIPDGETRKKIHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 IIGICVYVIPDGETRKKIHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240

Qy      241 FPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 FPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN 300

Qy      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRIFYRIQATR 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRIFYRIQATR 360

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Qy 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
 |||
 Db 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
 |||
 Db 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 |||
 Db 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
 |||
 Db 541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

RESULT 3

US-09-804-474A-2

; Sequence 2, Application US/09804474A

; Patent No. US20020119518A1

; GENERAL INFORMATION:

; APPLICANT: KODET, Stefan et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000891

; CURRENT APPLICATION NUMBER: US/09/804,474A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 921

; TYPE: PRT

; ORGANISM: Human

US-09-804-474A-2

Query Match 95.8%; Score 3093; DB 9; Length 921;

Best Local Similarity 100.0%; Pred. No. 4.2e-301;

Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGLVIL 60
 |||
 Db 1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGLVIL 60

Qy 61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120
 |||
 Db 61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120

Qy 121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180
 |||
 Db 121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF 180

Qy 181 IIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
 |||

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Db      181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qy      241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEETEGDHPKGIEMDGKMMNSHFLDGN 300
        |||
Db      241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEETEGDHPKGIEMDGKMMNSHFLDGN 300
Qy      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYYALSHQQKSRIFYRIQATR 360
        |||
Db      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYYALSHQQKSRIFYRIQATR 360
Qy      361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
        |||
Db      361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Qy      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
        |||
Db      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
Qy      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
        |||
Db      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qy      541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
        |||
Db      541 VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

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RESULT 4

US-10-054-680-2

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; Sequence 2, Application US/10054680
; Publication No. US20020132998A1
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: No. US20020132998A1e1 Human Ion Exchanger Proteins and
Polynucleotides Encoding the
; TITLE OF INVENTION: Same
; FILE REFERENCE: LEX-0301-USA
; CURRENT APPLICATION NUMBER: US/10/054,680
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: US 60/263,384
; PRIOR FILING DATE: 2001-01-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 921
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-054-680-2

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Query Match          95.8%; Score 3093; DB 13; Length 921;
Best Local Similarity 100.0%; Pred. No. 4.2e-301;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MAWLRLQPLTSAFLHFGVLTVFVFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
        |||
Db      1 MAWLRLQPLTSAFLHFGVLTVFVFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

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Qy	61	PIWYPENPSLGDKIDRVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIDRVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGDPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVEMANYYALSHQKSRFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQVEMANYYALSHQKSRFYRIQATR	360
Qy	361	MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRITSGARGTVIVPFRITVEGTAKGGGEDFEDTYGELEFKNDET	595
Db	541	VSESIGVMEVKVLRITSGARGTVIVPFRITVEGTAKGGGEDFEDTYGELEFKNDET	595

RESULT 5

US-10-114-153-4

; Sequence 4, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shenoy, Suresh

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter

; APPLICANT: Smithson, Glennnda

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li

; APPLICANT: Zerhusen, Bryan

; APPLICANT: Tchernev, Velizar

; APPLICANT: Gangolli, Esha

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; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 4
; LENGTH: 925
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-153-4

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Query Match          95.8%;  Score 3093;  DB 14;  Length 925;
Best Local Similarity 100.0%;  Pred. No. 4.2e-301;
Matches 595;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MAWLRLQPLTSAFLHFGVLTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
          |||
Db      1 MAWLRLQPLTSAFLHFGVLTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
          |||
Qy      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFRMASIEVITSQEREVTIKKPNGE 120

```

Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDI FEED EHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDI FEED EHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 6

US-10-275-116-2

; Sequence 2, Application US/10275116

; Publication No. US20030096312A1

; GENERAL INFORMATION:

; APPLICANT: Merck Patent GmbH

; TITLE OF INVENTION: No. US20030096312A1e1 natrium-calium exchanger protein

; FILE REFERENCE: HNCX3CWWS

; CURRENT APPLICATION NUMBER: US/10/275,116

; CURRENT FILING DATE: 2002-11-01

; NUMBER OF SEQ ID NOS: 2

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 927

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-275-116-2

Query Match 95.8%; Score 3093; DB 14; Length 927;

Best Local Similarity 100.0%; Pred. No. 4.2e-301;

Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIDRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRIFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRIFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 7

US-10-114-153-2

; Sequence 2, Application US/10114153

; Publication No. US20030185815A1

; GENERAL INFORMATION:

; APPLICANT: Padigar, Muralidhara

; APPLICANT: Shenoy, Suresh

; APPLICANT: Kekuda, Ramesh

; APPLICANT: Rastelli, Luca

; APPLICANT: Mezes, Peter

; APPLICANT: Smithson, Glennnda

; APPLICANT: Guo, Xiaojia

; APPLICANT: Gerlach, Valerie

; APPLICANT: Casman, Stacie

; APPLICANT: Boldog, Ferenc

; APPLICANT: Li, Li
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Gangolli, Esha
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Taupier, Raymond J. Jr.
 ; APPLICANT: Heyes, Melvyn
 ; APPLICANT: Ju, Jingfang
 ; APPLICANT: Peyman, John
 ; APPLICANT: Catterton, Elina
 ; APPLICANT: MacDougall, John
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: Stone, David
 ; APPLICANT: Mazur, Ann
 ; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
 NUCLEIC ACIDS
 ; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
 ; FILE REFERENCE: 21402-322A
 ; CURRENT APPLICATION NUMBER: US/10/114,153
 ; CURRENT FILING DATE: 2002-08-06
 ; PRIOR APPLICATION NUMBER: 60/281086
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281906
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/282020
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: 60/282930
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/283512
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/283444
 ; PRIOR FILING DATE: 2001-04-12
 ; PRIOR APPLICATION NUMBER: 60/283657
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283710
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283678
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/284234
 ; PRIOR FILING DATE: 2001-04-17
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 251
 ; SEQ ID NO 2
 ; LENGTH: 928
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-114-153-2

Query Match 95.8%; Score 3093; DB 14; Length 928;
 Best Local Similarity 100.0%; Pred. No. 4.2e-301;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFNLGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60

Qy      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE 120

Qy      121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAAFNMFI 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAAFNMFI 180

Qy      181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF 240

Qy      241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300

Qy      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQQKSRIFYRIQATR 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQQKSRIFYRIQATR 360

Qy      361 MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy      541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETIV 595
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETIV 595

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RESULT 8

US-09-804-474A-4

; Sequence 4, Application US/09804474A

; Patent No. US20020119518A1

; GENERAL INFORMATION:

; APPLICANT: KODET, Stefan et al

; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

; TITLE OF INVENTION: AND USES THEREOF

; FILE REFERENCE: CL000891

; CURRENT APPLICATION NUMBER: US/09/804,474A

; CURRENT FILING DATE: 2001-03-13

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 927

; TYPE: PRT
; ORGANISM: Rat
US-09-804-474A-4

Query Match 93.4%; Score 3016; DB 9; Length 927;
Best Local Similarity 97.1%; Pred. No. 2.3e-293;
Matches 578; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

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Qy      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
        ||||||||||||||||||||||||||||||||||||||||| |||| |||||||||||||||||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGDLRDVPSAGQNNESCSGSSDCKEGVIL 60

Qy     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
        ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db     61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120

Qy    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFI 180
        ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFI 180

Qy    181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
        |||||||||||||||||||||||||:|||||:|||||||||||||||||||||||||||
Db    181 IIGICVYVIPDGETRRIKHLRVFFVTAAWSVFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240

Qy    241 FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
        |||||||||||||||||||||||||:|||||:|||||||||||||||||||||||||||
Db    241 FPVCVLLAWVADKRLLFYKYMHKRYRTDKHRGIIIETEGEHPKGIEMDGKMMNSHFLDGN 300

Qy    301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRIFYRIQATR 360
        |:||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    301 LIPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRIFYRIQATR 360

Qy    361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
        |||||||||||||||||||||:|||||:|||||||||||||||||||||||||||
Db    361 MMTGAGNILKKHAAEQAKKTASMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVR 420

Qy    421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
        |||||:||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    421 KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy    481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
        |||||||||:|||| |||| ||| |||||||||||||||||||||||||||||||||||||
Db    481 FVRLSNVRVEEQLEEGMTPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy    541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET 595
        ||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDET 595
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RESULT 9

US-10-114-153-6

; Sequence 6, Application US/10114153
; Publication No. US20030185815A1
; GENERAL INFORMATION:
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Shenoy, Suresh
; APPLICANT: Kekuda, Ramesh

```

; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter
; APPLICANT: Smithson, Glennnda
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gerlach, Valerie
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Tchernev, Velizar
; APPLICANT: Gangolli, Esha
; APPLICANT: Vernet, Corine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Malyankar, Uriel
; APPLICANT: Patturajan, Meera
; APPLICANT: Miller, Charles
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Heyes, Melvyn
; APPLICANT: Ju, Jingfang
; APPLICANT: Peyman, John
; APPLICANT: Catterton, Elina
; APPLICANT: MacDougall, John
; APPLICANT: Edinger, Shlomit
; APPLICANT: Stone, David
; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: NOVEL ANTIBODIES THAT BIND TO ANTIGENIC POLYPEPTIDES,
NUCLEIC ACIDS
; TITLE OF INVENTION: ENCODING THE ANTIGENS, AND METHODS OF USE
; FILE REFERENCE: 21402-322A
; CURRENT APPLICATION NUMBER: US/10/114,153
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/281086
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282020
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/282930
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283512
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283444
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/283657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284234
; PRIOR FILING DATE: 2001-04-17
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 251
; SEQ ID NO 6
; LENGTH: 895
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-10-114-153-6

Query Match 91.1%; Score 2940; DB 14; Length 895;
Best Local Similarity 99.8%; Pred. No. 9.7e-286;
Matches 565; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      30 AEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL 89
      :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 SEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFL 61

Qy     90 GVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEIL 149
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 GVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEIL 121

Qy    150 LSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRGIKHLRVFFITA AW 209
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 LSLIEVCGHGFIAAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRGIKHLRVFFITA AW 181

Qy    210 SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDK 269
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 SIFAYIWLYMILAVFSPGVVQVWEGLLTLFFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDK 241

Qy    270 HRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRREMIRILKDLKQKHPE 329
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 HRGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRREMIRILKDLKQKHPE 301

Qy    330 KDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD 389
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 KDLDQLVEMANYYALSHQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTD 361

Qy    390 EPEDFISKVFFDPCSYQCLNCGAVLLTVVRKGGMSKTMVVDYKTEDGSANAGADYEFT 449
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 EPEDFISKVFFDPCSYQCLNCGAVLLTVVRKGGMSKTMVVDYKTEDGSANAGADYEFT 421

Qy    450 EGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP 509
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 EGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLP 481

Qy    510 RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTV 569
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    482 RAVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTV 541

Qy    570 EGTAKGGGEDFEDTYGELEFKNDETV 595
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Db    542 EGTAKGGGEDFEDTYGELEFKNDETV 567
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RESULT 10

US-09-901-419-2

; Sequence 2, Application US/09901419

; Patent No. US20020069421A1

; GENERAL INFORMATION:

; APPLICANT: The Curators of the University of Missouri

; TITLE OF INVENTION: LARGE SCALE EXPRESSION AND PURIFICATION OF RECOMBINANT

; TITLE OF INVENTION: PROTEINS

; FILE REFERENCE: UMO1531.1

; CURRENT APPLICATION NUMBER: US/09/901,419

; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/218,125
; PRIOR FILING DATE: 2000-01-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 970
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-901-419-2

Query Match 66.5%; Score 2147.5; DB 9; Length 970;
Best Local Similarity 69.4%; Pred. No. 5.7e-206;
Matches 422; Conservative 74; Mismatches 91; Indels 21; Gaps 8;

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Qy      1 MAWLRLQPLTSAFLHFGVLTFVLF--LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
      | | | | | : | | : | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MLQFSLSPTLSMGFHVIA MVALLFSHVDHISAETEMEGEGNETGE----CTGSYYCKKGV 56

Qy      59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN 118
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      57 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPN 116

Qy     119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIA GDLGPSTIVGSAAFNM 178
      | | | : | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db     117 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 176

Qy     179 FIIIGICVYVIPDGETR KIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL 238
      | | | | : | | | : | | | | | | | | | | | | | | | | | | | | | |
Db     177 FIIIALCVYVVPDGETR KIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEWEGLLTF 236

Qy     239 FFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIE TEGDHPKG---IEMDGKMMNSH 295
      | | | | : | | | : | | | | | | | | | | | | | | | | | | | | | |
Db     237 FFFPICVFAWVADRRLLFYKYVYKRYRAGKQ RGMIIIEHEGDRPSSKTEIEMDGKVNSH 296

Qy     296 ---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 348
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     297 VDSFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355

Qy     349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS YQC 407
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     356 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGT YQC 415

Qy     408 LENC GAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     416 LENC GTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

Qy     468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     476 IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVS---TLACLGSPSTATVTIFDDD 532

Qy     528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy     588 EFKNDETV 595
      | | : | | | |
```

RESULT 11

US-09-864-761-33429

; Sequence 33429, Application US/09864761

; Patent No. US20020048763A1

; GENERAL INFORMATION:

; APPLICANT: Penn, Sharron G.

; APPLICANT: Rank, David R.

; APPLICANT: Hanzel, David K.

; APPLICANT: Chen, Wensheng

; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
USEFUL FOR

; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

; FILE REFERENCE: Aeomica-X-1

; CURRENT APPLICATION NUMBER: US/09/864,761

; CURRENT FILING DATE: 2001-05-23

; PRIOR APPLICATION NUMBER: US 60/180,312

; PRIOR FILING DATE: 2000-02-04

; PRIOR APPLICATION NUMBER: US 60/207,456

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: US 09/632,366

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: GB 24263.6

; PRIOR FILING DATE: 2000-10-04

; PRIOR APPLICATION NUMBER: US 60/236,359

; PRIOR FILING DATE: 2000-09-27

; PRIOR APPLICATION NUMBER: PCT/US01/00666

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00667

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00664

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00669

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00665

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00662

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670

; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: US 60/234,687

; PRIOR FILING DATE: 2000-09-21

; PRIOR APPLICATION NUMBER: US 09/608,408

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: US 09/774,203

; PRIOR FILING DATE: 2001-01-29

; NUMBER OF SEQ ID NOS: 49117

; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 33429

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; LENGTH: 609
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007281.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.83
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.68
; OTHER INFORMATION: EST_HUMAN HIT: AW452398.1, EVALUE 1.00e-49
; OTHER INFORMATION: SWISSPROT HIT: P32418, EVALUE 0.00e+00
US-09-864-761-33429
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Query Match          66.4%; Score 2143.5; DB 9; Length 609;
Best Local Similarity 69.3%; Pred. No. 6.6e-206;
Matches 420; Conservative 76; Mismatches 89; Indels 21; Gaps 8;
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Qy      1 MAWLRLQPLTSAFLHFGGLVTFVLF--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV 58
      | | | | | : : | : : | | : | | : | | : | |
Db     11 MRRLSLSPTFSMGFHLTVSLLFSHVDHVIAETEMEGEGNETGE----CTGSYYCKKGV 66

Qy     59 ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPN 118
      | | | | | : : | | | | | : : | | | | | : : | | | | |
Db     67 ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQKEITIKKPN 126

Qy    119 GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNM 178
      | | | : | | : | | | | | | | | | | | : | | | | | | | |
Db    127 GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM 186

Qy    179 FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL 238
      | | | : | | | : | | | | | | | | | | | | | | | | | |
Db    187 FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF 246

Qy    239 FFFPVCVLLAWVADKRLLFYKYMHHKRYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH 295
      | | | : | | : | | | | | | | : : | | | | | | | | | |
Db    247 FFFPICVVFVAVADRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPSSKTEIEMDGKVNSH 306

Qy    296 ---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 348
      | | | | | | | | | | | : | | | | | | | | | : : : | | | |
Db    307 VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLSQQQ 365

Qy    349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
      | | | | | | | | : | | | | | | | | : | | | | | : | | |
Db    366 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVTENDPVSKIFFEQGTYQC 425

Qy    408 LENC GAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
      | | | | | | | : | | : | | : : | | : | | : | | | | | |
Db    426 LENC GTVALTIIRRGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGDTQKEIRVG 485

Qy    468 IIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
      | | | | | | | : | | | | : | | : : | | | | | | | | |
Db    486 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD 542

Qy    528 HAGIFTFECDTIHVSESIGVMEVKVLRRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
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          |||||  |||||:|||||  |||::|:||||:|||||  |||
Db      543 HAGFTFEEPVTHVSESIGIMEVKVLR TSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 602

Qy      588 EFKNDE 593
          ||:|
Db      603 EFQNDE 608

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RESULT 12

US-10-281-866-2

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; Sequence 2, Application US/10281866
; Publication No. US20030091570A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and compositions for the
; TITLE OF INVENTION: treatment and diagnosis of pain disorders using 46556
; FILE REFERENCE: MPI01-272P1RM
; CURRENT APPLICATION NUMBER: US/10/281,866
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/335,078
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-281-866-2

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Query Match          60.7%; Score 1961; DB 14; Length 921;
Best Local Similarity 65.7%; Pred. No. 3e-187;
Matches 371; Conservative 87; Mismatches 83; Indels 24; Gaps 6;

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Qy      40 STGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFM 99
          |||  |  |  | : ||:|:|  |::|  |||  |  | :|||:|:|  |||
Db      39 STG-----GCQGSYRCQPGVLLPVWEPDDPSLGDKAARAVVYFVAMVYMFLGVSIIADRFM 94

Qy      100 ASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHG 159
          |:|  |||:|:|:|  |  |||  |  |:|:|  |||  |||  |||  |||  |||  |||  |||
Db      95 AAIEVITSKEKEITITKANGETSVGTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHN 154

Qy      160 FIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYM 219
          |  ||:|  |||  |||  |||  |||:|  |:|:|  |||  ||:|  |||  |||:|  |||:
Db      155 FQAGELGPGTIVGSAAFNMFVVIACIYVIPAGESRRIKHLRVFFVTASWSIFAYVWLYL 214

Qy      220 ILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTDKHRGIIIEG 279
          |||  |||  |||  |||  |||  |||:  ||:|  |||  |||:|  |||  |||  |||  ||
Db      215 ILAVFSPGVVQVWEALLTLVFFPVCVFAWMADKRLLFYKYVYKRYRTDPRSGIIIGAEG 274

Qy      280 DHPKGIEMDGKMMNSHFLDGNL-----VPLEGKEVDESRRMIRILKDLKQKHPEKDLDQ 334
          |  ||  ||:|  |  :  |  |  |  |  |:|  |  |||:|  |||  |||:|  |||:
Db      275 DPPKSIELDGTFFVGAE-APGELGGLPGPAEARELDASRREVIQILKDLKQKHDPKDLEQ 333

Qy      335 LVE MANY YALSHQQKSRAF YRIQATRM MTGAGN I LK KHA AEQAKKASSMSEVHTDEPEDF 394
          ||  :|  |||  |||  |||  |||  |||:|  |||  |||:|  |||  |||  ||  :|
Db      334 LVGIANY YALLHQQKSRAF YRIQATRLMTGAGN VLR RHAADASRRAPAE GAGED E- DDG 392

```

Qy 395 ISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVV 454
 |::||:| | |||||:||||: ||: : | ||||:||||| ||:||||:||||:|
 Db 393 ASRIFFEPSLYHCLENCGSVLLSVTCQGGEGNSTFYVDYRTEDGSAKAGSDY EYSEGLTV 452

Qy 455 LKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQ-----PEEGMPPAIFNSLPLPR 510
 ||||| | :||||| ||||| ||||| |::: | | : | |:
 Db 453 FKPGETQKELRIGIIDDDIFEEDHFFVRLNLNRVGDAQGMFEPDGG-----GRPK 503

Qy 511 AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVE 570
 | :| :||||| |||||:|: |||| :| ::||:|:|:||||| :|:|:|:
 Db 504 GRLVAPLLATVTILDDDHAGIFSQDRLLHVSECMGTVDVRVVRSSGARGTVRLPYRTVD 563

Qy 571 GTAKGGGEDFEDTYGELEFKNDETV 595
 |||:| | :| | |||| :|:|:
 Db 564 GTARGGGVHYEDACGELEFGDDETM 588

RESULT 13

US-10-369-493-6319

; Sequence 6319, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 6319

; LENGTH: 890

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-369-493-6319

Query Match 37.1%; Score 1196.5; DB 15; Length 890;
 Best Local Similarity 47.6%; Pred. No. 2.2e-110;
 Matches 243; Conservative 97; Mismatches 150; Indels 21; Gaps 7;

Qy 87 MFLGVSIADRFMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAP 146
 ||||:|:|:|||||:||||| || : :|:| : :|:|:||||| |||||
 Db 1 MFLGISIVADRFMSSIEVITSMERTIVVKRPLDPMVQVRIWNTVSNLTLMALGSSAP 60

Qy 147 EILLSLIEVCCHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKIKHLRVFFIT 206
 ||||:| | || |||||:|||||:|:| || || || | : || || :|
 Db 61 EILLSIIEVIARGFEAGDLGPNTIVGSAAFNLFMIIAICVVVIPKGEIRRQKHLDFVCVT 120

Qy 207 AAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYR 266
 | ||:|:|:|:|:| || || :|| || || ||: | |::| :| :|: :|
 Db 121 ATWSVFAYVWLYLILAFFSPGEIEIWEGALTFIFFPLTVFTAYMADIKLIQNKFLPHRYR 180

QY 47 SCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVIT 106
| | : | | :: | : | : | | :: | | | | |

Db 2 SSSANLTCKNGILI-----PALETTTPRNAILYLAGLFYCFGLGIAIAADIFMCSIEQIT 54

Qy 107 SQEREVTIKKPNGETSTTT-----IRVWNETVSNLTLMALGSSAPEILLSLIEV 155
| : : | : | : : : | | : | | | | | | | | | | | | | : | :

Db 55 SATKKVKKQKKAGQLVAKEEDEEIDEQYDYVRIWNPTVANLTLMALGSSAPEILLSIIEI 114

Qy 156 CGHGFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRKHHLRVFFITAAWSIFAYI 215
| : | | | | | | | | | | | | | : | | : : : | | : | : | | |

Db 115 VGNGFKAGDLGPGTIVGSAAFNLFCSAICVFAV-GTQTKRIELRYRVFVVTAFFGT FayI 173

Qy 216 WLYMILAVFSPGVVQVWEGLLTLFFFFPVCVLLAWVADKRLLFYKYMHHKYRTD----- 268
| : : : | | : | | | | : | | | : : : | : : | | : |

Db 174 WVFLVLIVITPNVVDVWEAILTLLFFIILVVVSYAVDAQI-----WKKKKSSDLQEELEM 228

Qy 269 -KHRGIIIETEGDHPKGIEMDGKMMNSHFL----DGNLVPLEGKEVDESRR----- 314
: | | : | | : : | | : : : | | |

Db 229 AQHDGKV----DDQPEKLSDEIKKWASNLSLNKEENDVIVDATPSVDTVRRWTRTSISHTY 284

Qy 315 -----EMIRILKDLKQKHPEKDLQVLVEMANYYALSHQQ 348
| | : : | : : : : | | :

Db 285 PSLSDEDQAKILAYRVSRTMSHDRLYRIRAIRQLSSSWRKSEEEVLKMNQESTDSAS 344

Qy 349 KSRAF-----YRIQAT-----RMMTGAGNILLKHAAEQAK-----KASSM 383
: : | | : | | : | | : | | : : :

Db 345 RRKTFVEFSARVYRVDATDETVSLKIERKGNMESKFTVSYATVNGLAKKDLNFLFKSETL 404

Qy 384 ----SEVH-----TDEPEDFISKVFFDPC--SYQCLENCG 412
| : | | | | | | | : : | | |

Db 405 QFNPGELHKTISIQLINAAANWRPNDFYVHLKIQDVDED--SKICLGACNVAHVVENAG 462

Qy 413 AVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADY-EFTEGTVVLKPGETQKEFSVGIIDD 471
| | : | | : | | : | | : | : : | : | : : | |

Db 463 FSRSFVTRRGGLKKPLQVHYETEDVTAKQGDDYTAVKDGLGFEGQEYKEYIDIDVIDD 522

Qy 472 DIFEEDHEFFVRLSNVRIEEEQPEEGMPAIFNSLPLPRAVLASPCVATVTILDDDDH 528
: | : | | : | : : : | | : : | | : | | :

Db 523 KMDEKDEAFIIEI--LKVDE-----PGVSIGTRRKATITIIISDDN 560

RESULT 15

US-10-369-493-6149

; Sequence 6149, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

```
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6149
; LENGTH: 807
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6149
```

```
Query Match          19.6%; Score 633.5; DB 15; Length 807;
Best Local Similarity 29.1%; Pred. No. 7.9e-54;
Matches 174; Conservative 96; Mismatches 174; Indels 153; Gaps 18;
```

```
Qy      47 SCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVIT 106
      | | : | | |::      | : |      | : | | | |:: | | | | | | |
Db      2 SSSANLTCKNGILI-----PALETTPRNAILYLAGLFYCFLGIAIAADIFMCSIEQIT 54

Qy     107 SQEREVTIKKPNGETSTTT-----IRVWNETVSNLTLMALGSSAPEILLSLIEV 155
      | : : | : | | :      : | : | | | | | | | | | | | | | : | :
Db      55 SATKKVKKQKKAGQLVAKEEDEEIDEQYDYVRIWNPTVANLTLMALGSSAPEILLSIIEI 114

Qy     156 CGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGETRKHKLVRFFITAAWSIFAYI 215
      | : | | | | | | | | | | | | | | | | | : : : : | | : | : | | |
Db     115 VGNGFKAGDLGPGTIVGSAAFNLFCISAICVFAV-GTQTKRIELRVFVVTAFFGTFAIYI 173

Qy     216 WLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHKKYRTD----- 268
      | : : : | | : | | | | : | | | : | : : : | : :      | | : |
Db     174 WVFLVLIVITPNVVDVWEAILTLLFFIILVVVSYAVDAQI-----WKKKKSSDLQEELEM 228

Qy     269 -KHRGIIIIETEGDHPKGIEMDGMMNSHFL----DGNLVPLEGKEVDESRR----- 314
      : | | :      | | : : : | | :      : : :      | | | |
Db     229 AQHDGKV----DDQPEKLSDEIKKWASNLSLNKEENDVIVDATPSVDTVRRWTRTSISHTY 284

Qy     315 -----EMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ 348
      | | : : |      : : : : | | :
Db     285 PSLSDEDQAKILAYRVSRMTSHDRLYRIRAIRQLSSSWRKSEEEVLKMENQESTDSAS 344

Qy     349 KSRAF-----YRIQAT-----RMTTGAGNILKKHAAEQAK-----KASSM 383
      : : |      | | : | |      : | | : |      | : : :
Db     345 RRKTFVEFSARVYRVDATDETVSLKIERKGNMESKFTVSYATVNGLAKKDLNFLFKSETL 404

Qy     384 ----SEVH-----TDEPEDFISKVFFDPC--SYQCLENCG 412
      | : |      | | | | | : | : : | | |
Db     405 QFNPGELHKTISIQLINAANWRPNDFYVHLKIQDVDED--SKICLGACNVAHVVKENAG 462

Qy     413 AVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADY-EFTEGTVVLKPGETQKEFSVGIIDD 471
      | | : | | : | | : | | : | | : | : : | : | : : | |
Db     463 FSRSFVTRRGKLLKPLQVHYETEDVTAKQGDDYTAVKDGILGFEGQEYKYIDIDVIDD 522

Qy     472 DIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDH 528
      : | : | | : | : : : |      | : : | | : | | : | |
Db     523 KMDEKDEAFIIEI--LKVDE-----PGVSIGTRRKATITIIISDDN 560
```

```
Search completed: June 24, 2004, 16:17:31
Job time : 36.1986 secs
```

OM protein - protein search, using sw model

Run on: June 24, 2004, 16:06:37 ; Search time 32.9916 Seconds
(without alignments)
5929.434 Million cell updates/sec

Title: US-10-054-680-4
Perfect score: 3228
Sequence: 1 MAWLRLQPLTSAFLHFGLVT.....ADYGRGGQEDSRDGKASIG 620

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match Length DB	ID			Description

1	3093	95.8	924	4	Q96QG1	Q96qg1 homo sapien
2	3093	95.8	925	4	Q96QG2	Q96qg2 homo sapien
3	3012	93.3	595	11	Q9EPU8	Q9epu8 mus musculu
4	3012	93.3	921	11	Q7TS90	Q7ts90 mus musculu
5	3012	93.3	928	11	Q8VHJ8	Q8vhj8 mus musculu
6	2716	84.1	607	11	Q8BXN1	Q8bxn1 mus musculu
7	2315	71.7	771	4	Q86Y47	Q86y47 homo sapien
8	2157	66.8	934	6	O97801	O97801 macaca mula
9	2156.5	66.8	941	6	Q28662	Q28662 oryctolagus
10	2154.5	66.7	602	6	Q9TV05	Q9tv05 macaca mula
11	2136.5	66.2	941	6	Q9TS14	Q9ts14 oryctolagus
12	2133	66.1	934	11	Q9R238	Q9r238 rattus norv
13	2131	66.0	934	11	Q9WU30	Q9wu30 rattus norv
14	2129	66.0	957	11	Q9R239	Q9r239 rattus norv
15	2128.5	65.9	600	11	Q91ZJ7	Q91zj7 mus musculu
16	2126.5	65.9	600	11	Q9ET74	Q9et74 mus musculu
17	2124	65.8	962	11	Q924Y2	Q924y2 rattus norv
18	2124	65.8	969	11	Q9WU29	Q9wu29 rattus norv
19	2102	65.1	583	13	Q91850	Q91850 xenopus lae
20	2099.5	65.0	940	11	O35157	O35157 mus musculu
21	2030	62.9	968	13	Q9PT19	Q9pt19 oncorhynch
22	1962.5	60.8	921	11	Q8K596	Q8k596 mus musculu
23	1961	60.7	963	13	Q7T3T7	Q7t3t7 oreochromis
24	1846.5	57.2	706	11	Q8BxB3	Q8bxb3 mus musculu
25	1679	52.0	323	4	Q86TQ9	Q86tq9 homo sapien
26	1501	46.5	892	5	O02196	O02196 loligo opal
27	1339.5	41.5	950	5	Q9VDG5	Q9vdg5 drosophila
28	1339.5	41.5	950	5	Q24413	Q24413 drosophila
29	1328	41.1	950	5	O18367	O18367 drosophila
30	1288	39.9	925	5	O45630	O45630 caenorhabdi
31	1288	39.9	925	5	Q8MYP6	Q8myp6 caenorhabdi
32	1285.5	39.8	950	5	Q8I7I8	Q8i7i8 caenorhabdi
33	1285.5	39.8	975	5	Q8MYP5	Q8myp5 caenorhabdi
34	1278	39.6	254	13	Q9YH83	Q9yh83 gallus gall
35	1278	39.6	793	4	Q9H021	Q9h021 homo sapien
36	1160	35.9	880	5	Q21609	Q21609 caenorhabdi
37	1105.5	34.2	263	13	Q9YGE0	Q9yge0 oncorhynch
38	1046.5	32.4	263	13	Q9YH84	Q9yh84 gallus gall
39	1038	32.2	264	13	Q9YGE1	Q9yge1 oncorhynch
40	970.5	30.1	267	13	Q9YGE2	Q9yge2 oncorhynch
41	660	20.4	199	11	Q8R505	Q8r505 mus musculu
42	655	20.3	560	13	Q91849	Q91849 xenopus lae
43	633.5	19.6	807	5	Q21895	Q21895 caenorhabdi
44	523.5	16.2	171	11	Q8R504	Q8r504 mus musculu
45	519	16.1	215	11	Q9Z0T8	Q9z0t8 rattus norv

ALIGNMENTS

RESULT 1

Q96QG1

ID	Q96QG1	PRELIMINARY;	PRT;	924 AA.
AC	Q96QG1;			
DT	01-DEC-2001	(TrEMBLrel. 19, Created)		
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)		
DT	01-JUN-2003	(TrEMBLrel. 24, Last annotation update)		

DE Sodium/calcium exchanger SCL8A3.
GN SCL8A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Bortoluzzi S.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Gabellini N.;
RT "Characterization of the human SCL8A3 gene for solute carrier family
RT 8, member 3 (sodium/calcium exchanger).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ304853; CAC40985.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR004837; NaCa_Exmemb.
DR InterPro; IPR004836; Na_Ca_Ex.
DR Pfam; PF03160; Calx-beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMS; TIGR00845; caca; 1.
SQ SEQUENCE 924 AA; 102694 MW; A0A556B753998A07 CRC64;

Query Match 95.8%; Score 3093; DB 4; Length 924;
Best Local Similarity 100.0%; Pred. No. 9.2e-245;
Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADREFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADREFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRAFYRIQATR	360

Qy 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
 |||
 Db 361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420

Qy 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
 |||
 Db 421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480

Qy 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
 |||
 Db 481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540

Qy 541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
 |||
 Db 541 VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

RESULT 2

Q96QG2

ID Q96QG2 PRELIMINARY; PRT; 925 AA.
 AC Q96QG2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Sodium/calcium exchanger SCL8A3.
 GN SCL8A3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bortoluzzi S.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Gabellini N.;
 RT "Characterization of the human SCL8A3 gene for solute carrier family
 RT 8, member 3 (sodium/calcium exchanger).";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AJ304852; CAC40984.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 SQ SEQUENCE 925 AA; 102803 MW; 0CCF8DA0881C4FDA CRC64;

Query Match 95.8%; Score 3093; DB 4; Length 925;
 Best Local Similarity 100.0%; Pred. No. 9.2e-245;

Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQKSRFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRITSGARGTVIVPFRITVEGTAKGGGEDFEDTYGELEFKNDET	595
Db	541	VSESIGVMEVKVLRITSGARGTVIVPFRITVEGTAKGGGEDFEDTYGELEFKNDET	595

RESULT 3

Q9EPU8

ID Q9EPU8 PRELIMINARY; PRT; 595 AA.

AC Q9EPU8;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Sodium-calcium exchanger 3 (Fragment).

GN SLC8A3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.
 RA Sokolow S., Herchuelz A., Schurmans S.;
 RT "Mus musculus mRNA for sodium-calcium exchanger 3 (NCX3), partial
 RT sequence."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF321404; AAG42826.2; -.
 DR MGD; MGI:107976; Slc8a3.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 1.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 FT NON_TER 595 595
 SQ SEQUENCE 595 AA; 66200 MW; 8EF81CBC6EDB7854 CRC64;

Query Match 93.3%; Score 3012; DB 11; Length 595;
 Best Local Similarity 97.5%; Pred. No. 2.1e-238;
 Matches 580; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNCLRAEAGDSDGVP SAGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFVITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFVITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRIFYRIQATR	360
Db	301	FTPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEMANYALSHQQKSRIFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKTSSMSEVHTDEPEDFASKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540

```

Db          481  FVRLSNVRVEEEQLAEGMLPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qy          541  VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
Db          541  VSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDAYGELEFKNDETV 595

```

Q7TS90

Query Match 93.3%; Score 3012; DB 11; Length 921;
Best Local Similarity 97.5%; Pred. No. 4.1e-238;
Matches 580; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

```

      |||
Db      1 MAWLRLQPLTSAFLHFGLVTFVLFLNCLRAEAGDSGDVPSAGQNNESCSGSSDCKEGVIL 60
Qy      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
      |||
Db      61 PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE 120
Qy      121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
      |||
Db      121 TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI 180
Qy      181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
      |||
Db      181 IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF 240
Qy      241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
      |||
Db      241 FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qy      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQKSRAFYRIQATR 360
      |||
Db      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQKSRAFYRIQATR 360
Qy      361 MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
      |||
Db      361 MMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Qy      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
      |||
Db      421 KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
Qy      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
      |||
Db      481 FVRLSNVRVEEQQLAEGMLPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qy      541 VSESIGVMEVKVLRVTSRGARTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
      |||
Db      541 VSESIGVMEVKVLRVTSRGARTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

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RESULT 5

Q8VHJ8

ID Q8VHJ8 PRELIMINARY; PRT; 928 AA.

AC Q8VHJ8;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Sodium/calcium exchanger.

GN SLC8A3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Skeletal muscle;

RA Kraev A.;

Qy 541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDAYGELEFKNDETV 595

RESULT 6

Q8BXN1

ID Q8BXN1 PRELIMINARY; PRT; 607 AA.
 AC Q8BXN1;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Solute carrier family 8 (Fragment).
 GN SLC8A3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Retina;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK044636; BAC32013.1; -.
 DR MGD; MGI:107976; Slc8a3.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 1.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 FT NON_TER 607 607
 SQ SEQUENCE 607 AA; 68349 MW; 2762880AF5DEE19D CRC64;

Query Match 84.1%; Score 2716; DB 11; Length 607;
 Best Local Similarity 94.1%; Pred. No. 4.5e-214;
 Matches 524; Conservative 6; Mismatches 27; Indels 0; Gaps 0;

Qy 39 PSTGQNNESCSGSSDCKEGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRF 98
 | |: | : ||||||||||||||||||||||||||||
 Db 3 PVQGR TMSPVRGHQ TARRVSFCQLWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRF 62

Qy 99 MASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGH 158
 ||||||||||||||||||||||||||||||||||||||||
 Db 63 MASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGH 122

Qy 159 GFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETR KIKHLRVFFITAAWSIFAYIWLY 218
 ||||||||||||||||||||||||||||||||||||||||:||||||||||

Db 123 GFIAGDLGPSTIVGSAAFNMFIIGICVYVIPDGETRRIKHLRVFFVTAAWSIFAYIWLY 182

Qy 219 MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIETE 278
 |||

Db 183 MILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIETE 242

Qy 279 GDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEM 338
 |||

Db 243 GDHPKGIEMDGKMMNSHFLDGNFTPLEGKEVDESRRMIRILKDLKQKHPEKDLDQLVEM 302

Qy 339 ANYYALSHQQKSRIFYRIQATRMMTGAGNILLKHAEEQAKKASSMSEVHTDEPEDFISKV 398
 |||

Db 303 ANYYALSHQQKSRIFYRIQATRMMTGAGNILLKHAEEQAKKTSSMSEVHTDEPEDFASKV 362

Qy 399 FFDPCSQCLENCGAVLLTVVRKGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPG 458
 |||

Db 363 FFDPCSQCLENCGAVLLTVVRKGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPG 422

Qy 459 ETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCV 518
 |||

Db 423 ETQKEFSVGIIDDDIFEEDHFFVRLSNVRVEEQLAEGMLPAILNSLPLPRAVLASPCV 482

Qy 519 ATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGE 578
 |||

Db 483 ATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGE 542

Qy 579 DFEDTYGELEFKNDETV 595
 |||

Db 543 DFEDAYGELEFKNDETV 559

RESULT 7

Q86Y47

ID Q86Y47 PRELIMINARY; PRT; 771 AA.

AC Q86Y47;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Na⁺/Ca²⁺ exchanger isoform 4 (Fragment).

GN NACAIS4.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Lindgren R.M., Bongcam-Rudloff E., Nister M., Heller S.;

RT "Homo sapiens partial mRNA for Na⁺/Ca²⁺ exchanger isoform 4.";

RL Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AJ508602; CAD48420.1; -.

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.

DR GO; GO:0006816; P:calcium ion transport; IEA.

DR InterPro; IPR003644; Calx_beta.

DR InterPro; IPR004837; NaCa_Exmemb.

DR InterPro; IPR004836; Na_Ca_Ex.

DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 1.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 FT NON TER 1 1
 SQ SEQUENCE 771 AA; 86146 MW; A204AAA48A52ED8B CRC64;

Query Match 71.7%; Score 2315; DB 4; Length 771;
 Best Local Similarity 99.6%; Pred. No. 5.5e-181;
 Matches 443; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	151	SLIEVCGHGFIAGDLGPSTIVGSAAFMFIIIGICVYVIPDGETRRIKHLRVFFITAAWS	210
Db	1	SLIEVCGHGFIAGDLGPSTIVGSAAFMFIIIGICVYVIPDGETRRIKHLRVFFITAAWS	60
Qy	211	IFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKH	270
Db	61	IFAYIWLYMILAVFSPGVVQVWEGLLTLFFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKH	120
Qy	271	RGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPEK	330
Db	121	RGIIIETEGDHPKGIEMDGKMMNSHFLDGNLVPLEGKEVDESRRMIRILKDLKQKHPEK	180
Qy	331	DLQDLVEMANYALSHQKSRIFYRIQATRMGTAGNIIKKHAAEQAKKASSMSEVHTDE	390
Db	181	DLQDLVEMANYALSHQKSRIFYRIQATRMGTAGNIIKKHAAEQAKKASSMSEVHTDE	240
Qy	391	PEDFISKVFFDPCSYQCLNCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTE	450
Db	241	PEDFISKVFFDPCSYQCLNCGAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTE	300
Qy	451	GTVVLKPGETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR	510
Db	301	GTVVLKPRETQKEFSVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR	360
Qy	511	AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVE	570
Db	361	AVLASPCVATVTILDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVE	420
Qy	571	GTAKGGGEDFEDTYGELEFKNDET	595
Db	421	GTAKGGGEDFEDTYGELEFKNDET	445

RESULT 8

O97801

ID O97801 PRELIMINARY; PRT; 934 AA.
 AC O97801;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Sodium-calcium exchanger isoform NCX1.3.
 GN NCX1.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=99175198; PubMed=10075718;
 RA Li X.F., Lytton J.;
 RT "A circularized sodium-calcium exchanger exon 2 transcript.";
 RL J. Biol. Chem. 274:8153-8160(1999).
 DR EMBL; AF107593; AAD04173.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAJ_2; 1.
 SQ SEQUENCE 934 AA; 104331 MW; 2A228DA30254BBC2 CRC64;

Query Match 66.8%; Score 2157; DB 6; Length 934;
 Best Local Similarity 68.7%; Pred. No. 6.9e-168;
 Matches 426; Conservative 76; Mismatches 90; Indels 28; Gaps 9;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLF--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV	58
		: : : : : :	
Db	1	MRRLSLSPTFSMGFHLVIVALLFSHVDYVIAETEMEGEGNETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN	118
		: : : : : :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIA GD LGPSTIVGSAAFNM	178
		: : : :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGD LGPSTIVGSAAFNM	176
Qy	179	FIIIGICVYVIPDGETR K I K H L R V F F I T A A W S I F A Y I W L Y M I L A V F S P G V V Q V W E G L L T L	238
		: : : : :	
Db	177	FIIIALCVYVVPDGETR K I K H L R V F F V T A A W S I F A Y T W L Y I I L S V I S P G V V E V W E G L L T F	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYM HK KYRTDKHRGII I E T E G D H P K G --- I E M D G K M M N S H	295
		: : : : : :	
Db	237	FFFPICVVFVAVVADRRLLFYKYVYKRYRAGKQ R G M I I E H E G D R P S S K T E I E M D G K V V N S H	296
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ	348
		: : : :	
Db	297	VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355
Qy	349	KSRAFYRIQATRM MT GAGN I L K K H A A E Q A K K A S S M S E V H T D E P E - D F I S K V F F D P C S Y Q C	407
		: : : : : : : :	
Db	356	KSRAFYRIQATRLMTGAGN I L K R H A A D Q A R K A V S M H E V N T E V T E N D P V S K I F F E Q G T Y Q C	415

QY 408 LENC GAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
 ||||| | ||::||::||::||::||::||::||::||::||::||::||::||::||::||
 Db 416 LENC GTVALTIIRRGDDLNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

QY 468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
 ||||| ||||::| | ||||:: | |::| | | | | | | | | | | | | | | | | |
 Db 476 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD 532

QY 528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

QY 588 EFKNDETV-----CDRQE 600
 ||::||| | ||:|
 Db 593 EFQNDEIVKIITIRIFDREE 612

RESULT 9

Q28662

ID Q28662 PRELIMINARY; PRT; 941 AA.
 AC Q28662;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Renal Na/Ca exchanger NACA-2.
 GN NCX1.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=92321271; PubMed=1621815;
 RA Reilly R.F., Shugrue C.A.;
 RT "cDNA cloning of a renal Na(+)-Ca2+ exchanger.";
 RL Am. J. Physiol. 262:F1105-F1109(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Reilly R.F., Shugrue C.A.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U52665; AAA97928.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAJ_2; 1.
 SQ SEQUENCE 941 AA; 105128 MW; 7E11396DE70A4084 CRC64;

Query Match 66.8%; Score 2156.5; DB 6; Length 941;
 Best Local Similarity 68.8%; Pred. No. 7.7e-168;
 Matches 421; Conservative 77; Mismatches 87; Indels 27; Gaps 9;

Qy	8	PLTSAFLHFGLVTFVLF-LNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIWYPE	66
		: : : : : : : : : : :	
Db	9	PFSMGFHLAIVALFFFRVDHVS AETEME GEGNETGE----CTGSYYCKKG VILPIWEPQ	64
Qy	67	NPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGETSTTTI	126
		: : : : : :	
Db	65	DPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSSIEVITSQEKEITIKKPNGETTKTTV	124
Qy	127	RVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIA GDLGPSTIVGSAAFNMFIIGICV	186
		: : :	
Db	125	RIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIALCV	184
Qy	187	YVIPDGETRKIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFFFPVCVL	246
		: : :	
Db	185	YVVPDGETRKIKHLRVFFVTAAWSIFAYTWLYIILSVISPGIVEVWEGLLTFFFFPICVV	244
Qy	247	LAWVADKRLLFYKYMHHKRYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH---FLDGN	300
		: : :	
Db	245	FAWVADRRLLFYKYVYKRYRAGKQ RGMII EHEGDRPSSKTEIEMDGKVVNSHVDNFLDGA	304
Qy	301	LVPLEGKEVD----ESRREMIRILKDLKQKHPEKDL DQLVEMANYYALSHQQKSRAFYRI	356
		: : : : : :	
Db	305	LV-LDVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQKSRAFYRI	363
Qy	357	QATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLENCGAVL	415
		: : :	
Db	364	QATRLMTGAGNILKRHAADQARKAVSMHEVNTEMAENDPVSKIFFEQGT YQCLENCGTVA	423
Qy	416	LTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFE	475
		: : : : : : :	
Db	424	LTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVGIIDDDIFE	483
Qy	476	EDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD HAGIFTFE	535
		: : : :	
Db	484	EDENFLVHLSNVKVSSETSEDGILEANHIS---TLACLGSPCTATVTIFDDDHAGIFTFE	540
Qy	536	CDTIHVSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
		: : : :	
Db	541	ESVTHVSESIGIMEVKVLR TSGARGNVIVPYKTIEGTARGGGEDFEDTCGELEFQND EIV	600
Qy	596	-----CDRQE	600
		:	
Db	601	KIITIRIFDREE	612

RESULT 10

Q9TV05

ID Q9TV05 PRELIMINARY; PRT; 602 AA.

AC Q9TV05;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Sodium-calcium exchanger circular exon 2 transcript.
 GN NCX1.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=99175198; PubMed=10075718;
 RA Li X.F., Lytton J.;
 RT "A circularized sodium-calcium exchanger exon 2 transcript.";
 RL J. Biol. Chem. 274:8153-8160(1999).
 DR EMBL; AF109888; AAD04174.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 1.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAJ_2; 1.
 SQ SEQUENCE 602 AA; 67369 MW; F46C6D8D1D32040E CRC64;

Query Match 66.7%; Score 2154.5; DB 6; Length 602;
 Best Local Similarity 69.6%; Pred. No. 5.7e-168;
 Matches 423; Conservative 75; Mismatches 89; Indels 21; Gaps 8;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLF--LNGLRAEAGSGDVPSTGQNNESCSGSSDCKEGV	58
		: : : : : :	
Db	1	MRRLSLSPTFSMGFHLIVIVALLFSHVDYVIAETEMEGETNETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN	118
		: : : : : : :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFAGDLGPSTIVGSAAAFNM	178
		: : : :	
Db	117	GETTKTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAAFNM	176
Qy	179	FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL	238
		: : :	
Db	177	FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIIEGTHPKG---IEMDGKMMNSH	295
		: : : : : : : :	
Db	237	FFFPICVFAWVADRRLLFYKYVYKRYRAGKQKGMIEHEGDRPSSKTEIEMDGKVVNSH	296
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQLVEMANYALSHQQ	348
		: : : : : : :	
Db	297	VENFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355

Qy 349 KSRIFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
 |||||:|||||:|:|:| || ||:| | | :||:|: | |||
 Db 356 KSRIFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVTENDPVSKIFFEQGTYQC 415

Qy 408 LENC GAVLLTVVRKGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
 |||| | ||:|:|:|:| :|:|:|:|:|:|:|:|:|:|:|:| ||| ||
 Db 416 LENC GTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

Qy 468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
 |||||:| | |||:| | |:| | | | | | | | | | | | | |
 Db 476 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---TLACLGSPSTATVTIFDDD 532

Qy 528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRFTVEGTAKGGGEDFEDTYGEL 587
 ||||| | |||||:||||| ||||:|:|:|:|:|:|:| |||
 Db 533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy 588 EFKNDETV 595
 ||:| | |
 Db 593 EFQNDEIV 600

RESULT 11

Q9TS14

ID Q9TS14 PRELIMINARY; PRT; 941 AA.
 AC Q9TS14;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE NA/CA exchanger isoform NACA6.
 OS *Oryctolagus cuniculus* (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; *Oryctolagus*.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94148976; PubMed=8106495;
 RA Kofuji P., Lederer W.J., Schulze D.H.;
 RT "Mutually exclusive and cassette exons underlie alternatively spliced
 RT isoforms of the Na/Ca exchanger."
 RL J. Biol. Chem. 269:5145-5149(1994).
 DR PIR; B53335; B53335.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAJ_2; 1.
 SQ SEQUENCE 941 AA; 104995 MW; AEC76774E9E81815 CRC64;

Query Match 66.2%; Score 2136.5; DB 6; Length 941;

Qy 465 SVGIIDDDIFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
 |||||:| | ||||: | |:| | : | | || ||:|
 Db 473 RVGIIDDDIFEEDENFLVHLSNVRVSSEVSEDG----ILDSNHVSAIACLGSPNTATITI 528

Qy 524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
 |||||:| |||||:||||| ||:|:|:|:|:|:|:|:|
 Db 529 FDDDHAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDT 588

Qy 584 YGELEFKNDETV-----CDRQE 600
 ||||:| | ||:
 Db 589 CGELEFQNDIVKIITIRIFDREE 612

RESULT 13

Q9WU30

ID Q9WU30 PRELIMINARY; PRT; 934 AA.
 AC Q9WU30;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Na+/Ca2+-exchanging protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RA Unlap M.T., Bell P.D.;
 RT "cDNA cloning of two Na+/Ca2+ exchangers in mesangial cells from
 RT Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats."
 RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF109166; AAD23389.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
 DR GO; GO:0006816; P:calcium ion transport; IEA.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR001623; DnaJ_N.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 DR PROSITE; PS50076; DNAJ_2; 1.
 SQ SEQUENCE 934 AA; 104210 MW; 054D06E9179098B5 CRC64;

Query Match 66.0%; Score 2131; DB 11; Length 934;
 Best Local Similarity 67.8%; Pred. No. 9.5e-166;
 Matches 423; Conservative 73; Mismatches 88; Indels 40; Gaps 10;

Qy 4 LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGSGDVPSTGQNNESCSGSSDCK 55
 ||| : | || | | || ||: |:|| ||
 Db 2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53

RT "cDNA cloning of two Na⁺/Ca²⁺ exchangers in mesangial cells from
RT Dahl/Rapp salt-sensitive (S) and salt-resistant (R) rats."
RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF109164; AAD23387.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005432; F:calcium:sodium antiporter activity; IEA.
DR GO; GO:0006816; P:calcium ion transport; IEA.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR001623; DnaJ_N.
DR InterPro; IPR004837; NaCa_Exmemb.
DR InterPro; IPR004836; Na_Ca_Ex.
DR Pfam; PF03160; Calx-beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMs; TIGR00845; caca; 1.
DR PROSITE; PS50076; DNAJ_2; 1.
SQ SEQUENCE 957 AA; 106724 MW; 7A146630451EAA7E CRC64;

Query Match 66.0%; Score 2129; DB 11; Length 957;
Best Local Similarity 67.8%; Pred. No. 1.4e-165;
Matches 423; Conservative 72; Mismatches 89; Indels 40; Gaps 10;

Qy	4	LRLQPLTSAFLHFGLVTFVLFL-----NGLRAEAGGSGDVPSTGQNNESCSGSSDCK	55
		: : : :	
Db	2	LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK	53
Qy	56	EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK	115
		: :: ::: : : :	
Db	54	KGVILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIIADRFMSIEVITSQEKEITIK	113
Qy	116	KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAA	175
		: : : :	
Db	114	KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFAGDLGPSTIVGSAA	173
Qy	176	FNMFIIGICVYVIPDGETRGIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGL	235
		: : : : : :	
Db	174	FNMFIILALCVYVVPDGETRGIKHLRVFFVTAAWSIFAYTWLYIFLSVSSPGVVEVWEGL	233
Qy	236	LTLEFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKG---IEMDGKMM	292
		: : : : : : :	
Db	234	LTFFFPICVFAWVADRRLFYKYVYKRYRAGKQGRGMIIEHEGDRPASKTEIEMDGKV	293
Qy	293	NSH---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYALS	345
		: : : :: : :	
Db	294	NSHVDNFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS	352
Qy	346	HQQKSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS	404
		: : : : : : : :	
Db	353	QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT	412
Qy	405	YQCLENCGAVLLTVVRKGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF	464
		:: : : : : ::: : : : : : : : : :	
Db	413	YQCLENCGTVALTIIRRGDLTNTVSVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI	472
Qy	465	SVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI	523
		: : : : :	

OM protein - protein search, using sw model

Run on: June 24, 2004, 15:55:42 ; Search time 11.6677 Seconds
 (without alignments)
 2766.900 Million cell updates/sec

Title: US-10-054-680-4
 Perfect score: 3228
 Sequence: 1 MAWLRLQPLTSAFLHFGLVT.....ADYGRRGGQEDSRDGKASIG 620

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	3093	95.8	927	1	NAC3_HUMAN	P57103 homo sapien
2	3016	93.4	927	1	NAC3_RAT	P70549 rattus norv
3	2159.5	66.9	970	1	NAC1_CANFA	P23685 canis famil
4	2152.5	66.7	970	1	NAC1_FELCA	P48767 felis silve
5	2147.5	66.5	970	1	NAC1_BOVIN	P48765 bos taurus
6	2146.5	66.5	973	1	NAC1_HUMAN	P32418 homo sapien
7	2142.5	66.4	970	1	NAC1_CAVPO	P48766 cavia porce
8	2135.5	66.2	971	1	NAC1_RAT	Q01728 rattus norv
9	2115.5	65.5	970	1	NAC1_MOUSE	P70414 mus musculu
10	1961	60.7	921	1	NAC2_HUMAN	Q9upr5 homo sapien
11	1954.5	60.5	921	1	NAC2_RAT	P48768 rattus norv
12	209.5	6.5	663	1	NKX1_CHICK	Q9ial8 gallus gall
13	203.5	6.3	661	1	NKX2_HUMAN	Q9ui40 homo sapien
14	203	6.3	1181	1	NKX1_RAT	Q9qzm6 rattus norv
15	201.5	6.2	670	1	NKX2_RAT	O54701 rattus norv
16	199.5	6.2	651	1	NKX2_CHICK	Q9ial7 gallus gall
17	194.5	6.0	1216	1	NKX1_BOVIN	Q28139 bos taurus

18	193	6.0	605	1	NKX4_HUMAN	Q8nff2	homo sapien
19	189	5.9	605	1	NKX4_MOUSE	Q8cgq8	mus musculu
20	186.5	5.8	644	1	NKX3_HUMAN	Q9hc58	homo sapien
21	181	5.6	624	1	NKX3_RAT	Q9epq0	rattus norv
22	179	5.5	645	1	NKX3_MOUSE	Q99pd7	mus musculu
23	178	5.5	1099	1	NKX1_HUMAN	O60721	homo sapien
24	162.5	5.0	856	1	NCKX_DROME	Q9u6a0	drosophila
25	141.5	4.4	572	1	YKT4_CAEEL	P34315	caenorhabdi
26	132	4.1	1807	1	ITB4_RAT	Q64632	rattus norv
27	131	4.1	590	1	YKTA_CAEEL	P34322	caenorhabdi
28	126.5	3.9	1822	1	ITB4_HUMAN	P16144	homo sapien
29	110	3.4	3358	1	PGCV_MOUSE	Q62059	mus musculu
30	108	3.3	673	1	COAT_PAVBO	P07297	bovine parv
31	107	3.3	548	1	CH60_EHRSE	O32606	ehrlichia s
32	107	3.3	649	1	TOP3_SALTI	Q8z6f5	salmonella
33	106.5	3.3	1036	1	YAN2_SCHPO	Q10068	schizosacch
34	106	3.3	649	1	TOP3_SALTY	P40687	salmonella
35	105.5	3.3	548	1	CH60_EHRR1	P48214	ehrlichia r
36	105	3.3	402	1	PGK_CHLPN	Q9z7m5	chlamydia p
37	104.5	3.2	686	1	MXIA_SHIFL	P35533	shigella fl
38	104.5	3.2	1828	1	MAP2_MOUSE	P20357	mus musculu
39	103.5	3.2	988	1	TNP6_ENTFC	Q06238	enterococcu
40	102.5	3.2	2009	1	CIN1_HUMAN	P35498	homo sapien
41	101.5	3.1	989	1	RPOC_LEUME	P94892	leuconostoc
42	100	3.1	510	1	GPMI_CLOAB	Q97153	clostridium
43	100	3.1	1065	1	SEC8_YEAST	P32855	saccharomyc
44	99.5	3.1	1018	1	SYI_ARCFU	O29622	archaeoglob
45	98.5	3.1	558	1	RTF1_YEAST	P53064	saccharomyc

ALIGNMENTS

RESULT 1

NAC3_HUMAN

ID NAC3_HUMAN STANDARD; PRT; 927 AA.
AC P57103; Q8IUE9; Q8IUFO; Q8NFI7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein
DE 3).
GN SLC8A3 OR NCX3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 2; 3 AND 4).
RX MEDLINE=22294016; PubMed=12406570;
RA Gabellini N., Bortoluzzi S., Danieli G.A., Carafoli E.;
RT "The human SLC8A3 gene and the tissue-specific Na+/Ca2+ exchanger 3
RT isoforms.";
RL Gene 298:1-7(2002).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=22447378; PubMed=12558991;

RA Gabellini N., Bortoluzzi S., Danieli G.A., Carafoli E.;
 RT "Control of the Na⁺/Ca²⁺ exchanger 3 promoter by cyclic adenosine
 RT monophosphate and Ca²⁺ in differentiating neurons."
 RL J. Neurochem. 84:282-293(2003).
 RN [3]
 RP SEQUENCE OF 1-595 FROM N.A.
 RA Kraev A.S., Chumakov I.M., Carafoli E.;
 RT "The organization of the human gene of the sodium-calcium exchanger."
 RL Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores (By similarity).
 CC -!- ENZYME REGULATION: By intracellular calcium ions (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=3; Synonyms=NCX3.3;
 CC IsoId=P57103-1; Sequence=Displayed;
 CC Name=2; Synonyms=NCX3.2;
 CC IsoId=P57103-2; Sequence=VSP_008116;
 CC Name=4; Synonyms=NCX3.4;
 CC IsoId=P57103-3; Sequence=VSP_008117, VSP_008118;
 CC -!- TISSUE SPECIFICITY: Isoform 2 is expressed in brain and skeletal
 CC muscle; Isoform 3 is expressed in excitable cells of brain, retina
 CC and skeletal muscle; Isoform 4 is expressed in skeletal muscle.
 CC -----
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 DR EMBL; AF510501; AAN60790.1; -.
 DR EMBL; AF510502; AAN60791.1; -.
 DR EMBL; AF510503; AAN60792.1; -.
 DR EMBL; AF508982; AAM90955.1; -.
 DR EMBL; X93017; -; NOT_ANNOTATED_CDS.
 DR Genew; HGNC:11070; SLC8A3.
 DR MIM; 607991; -.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 1.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat; Alternative splicing.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 927 SODIUM/CALCIUM EXCHANGER 3.
 FT DOMAIN 31 73 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 74 94 POTENTIAL.
 FT DOMAIN 95 147 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 148 168 POTENTIAL.

FT	DOMAIN	169	169	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	170	190	POTENTIAL.
FT	DOMAIN	191	202	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	203	223	POTENTIAL.
FT	DOMAIN	224	230	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	231	251	POTENTIAL.
FT	DOMAIN	252	726	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	727	747	POTENTIAL.
FT	DOMAIN	748	754	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	755	775	POTENTIAL.
FT	DOMAIN	776	778	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	779	799	POTENTIAL.
FT	DOMAIN	800	828	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	829	849	POTENTIAL.
FT	DOMAIN	850	860	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	861	881	POTENTIAL.
FT	DOMAIN	882	903	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	904	924	POTENTIAL.
FT	DOMAIN	925	927	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	253	272	CALMODULIN-BINDING (BY SIMILARITY).
FT	REPEAT	140	180	ALPHA-1.
FT	REPEAT	399	470	BETA-1.
FT	REPEAT	534	604	BETA-2.
FT	REPEAT	796	832	ALPHA-2.
FT	CARBOHYD	45	45	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	823	823	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	630	635	Missing (in isoform 2).
FT				/FTId=VSP_008116.
FT	VARSPLIC	596	620	KTIRVKIVDEEYERQENFFIALGE -> CDRQEADYGRRG
FT				GQEDSRDGKASIG (in isoform 4).
FT				/FTId=VSP_008117.
FT	VARSPLIC	621	927	Missing (in isoform 4).
FT				/FTId=VSP_008118.
SQ	SEQUENCE	927 AA;	103009 MW;	7B43CB6A9D77615E CRC64;

Query Match 95.8%; Score 3093; DB 1; Length 927;
 Best Local Similarity 100.0%; Pred. No. 6.6e-216;
 Matches 595; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIDRVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIDRVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFI	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKYRTDKHRIIETEGDHPKGIEMDGKMMNSHFLDGN	300

```

Db      241 FPVCVLLAWVADKRLLFYKYMHHKKYRTDKHRGIIIETEGDHPKGIEMDGKMMNSHFLDGN 300
Qy      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRIFYRIQATR 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYYALSHQQKSRIFYRIQATR 360
Qy      361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR 420
Qy      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      421 KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF 480
Qy      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH 540
Qy      541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 VSESIGVMEVKVLR TSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV 595

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RESULT 2

NAC3_RAT

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ID      NAC3_RAT          STANDARD;          PRT;    927 AA.
AC      P70549;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Sodium/calcium exchanger 3 precursor (Na(+)/Ca(2+)-exchange protein
DE      3).
GN      SLC8A3 OR NCX3.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_TaxID=10116;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Sprague-Dawley; TISSUE=Brain;
RX      MEDLINE=96394663; PubMed=8798769;
RA      Nicoll D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
RA      Philipson K.D.;
RT      "Cloning of a third mammalian Na+-Ca2+ exchanger, NCX3.";
RL      J. Biol. Chem. 271:24914-24921(1996).
CC      -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC      coupling. Ca(2+) is extruded from the cell during relaxation so as
CC      to prevent overloading of intracellular stores.
CC      -!- ENZYME REGULATION: By intracellular calcium ions.
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -!- TISSUE SPECIFICITY: Expression restricted to brain and skeletal
CC      muscle.

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CC      the European Bioinformatics Institute. There are no restrictions on its
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-----
DR EMBL; U53420; AAC52817.1; -.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR004836; Na_Ca_Ex.
DR InterPro; IPR004837; NaCa_Exmemb.
DR Pfam; PF03160; Calx-beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMs; TIGR00845; caca; 1.
KW Transport; Antiport; Calcium transport; Sodium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW Calmodulin-binding; Repeat.
FT SIGNAL      1      30      POTENTIAL.
FT CHAIN       31     927     SODIUM/CALCIUM EXCHANGER 3.
FT DOMAIN      31      73     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM    74      94     POTENTIAL.
FT DOMAIN      95     147     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   148     168     POTENTIAL.
FT DOMAIN     169     169     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   170     190     POTENTIAL.
FT DOMAIN     191     202     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   203     223     POTENTIAL.
FT DOMAIN     224     230     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   231     251     POTENTIAL.
FT DOMAIN     252     726     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   727     747     POTENTIAL.
FT DOMAIN     748     754     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   755     775     POTENTIAL.
FT DOMAIN     776     778     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   779     799     POTENTIAL.
FT DOMAIN     800     828     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   829     849     POTENTIAL.
FT DOMAIN     850     860     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   861     881     POTENTIAL.
FT DOMAIN     882     903     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   904     924     POTENTIAL.
FT DOMAIN     925     927     CYTOPLASMIC (POTENTIAL).
FT DOMAIN     253     272     CALMODULIN-BINDING (BY SIMILARITY).
FT REPEAT     140     180     ALPHA-1.
FT REPEAT     399     470     BETA-1.
FT REPEAT     534     604     BETA-2.
FT REPEAT     796     832     ALPHA-2.
FT DOMAIN     645     648     POLY-GLU.
FT CARBOHYD     45      45     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD    823     823     N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE   927 AA;  103162 MW;  EAB35F9620DBE69E CRC64;
  
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Query Match 93.4%; Score 3016; DB 1; Length 927;
 Best Local Similarity 97.1%; Pred. No. 2.5e-210;
 Matches 578; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVIL 60
 |||

Db	1	MAWLRLQPLTSAFLHFGLVTFVLFLNGLRAEAGDLRDVPSAGQNNESCSGSSDCKEGVIL	60
Qy	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Db	61	PIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIKKPNGE	120
Qy	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Db	121	TSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMF	180
Qy	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Db	181	IIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTLFF	240
Qy	241	FPVCVLLAWVADKRLLFYKYMHHKRYRTDKHRGIIETEGDHPKGIEMDGKMMNSHFLDGN	300
Db	241	FPVCVLLAWVADKRLLFYKYMHHKRYRTDKHRGIIETEGEHPKGIEMDGKMMNSHFLDGN	300
Qy	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQQKSRAFYRIQATR	360
Db	301	LVPLEGKEVDESRRMIRILKDLKQKHPEKDLQLVEMANYALSHQQKSRAFYRIQATR	360
Qy	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Db	361	MMTGAGNILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVR	420
Qy	421	KGGDMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Db	421	KGGDISKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHF	480
Qy	481	FVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Db	481	FVRLSNVRVEEQLEEGMTPAILNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTIH	540
Qy	541	VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595
Db	541	VSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKNDETV	595

RESULT 3

NAC1_CANFA

ID NAC1_CANFA STANDARD; PRT; 970 AA.

AC P23685;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein 1).

GN SLC8A1.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RX MEDLINE=91047958; PubMed=1700476;

RA Nicoll D.A., Longoni S., Philipson K.D.;
 RT "Molecular cloning and functional expression of the cardiac
 RT sarcolemmal Na(+)-Ca2+ exchanger.";
 RL Science 250:562-565(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=92152737; PubMed=1785844;
 RA Nicoll D.A., Philipson K.D.;
 RT "Molecular studies of the cardiac sarcolemmal sodium-calcium
 RT exchanger.";
 RL Ann. N.Y. Acad. Sci. 639:181-188(1991).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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 CC -----
 DR EMBL; M57523; AAA62766.1; -.
 DR PIR; A36417; A36417.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
 FT DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 POTENTIAL.
 FT DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 168 188 POTENTIAL.
 FT DOMAIN 189 199 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 200 222 POTENTIAL.
 FT DOMAIN 223 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 249 POTENTIAL.
 FT DOMAIN 250 769 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 770 789 POTENTIAL.
 FT DOMAIN 790 796 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 797 819 POTENTIAL.
 FT DOMAIN 820 821 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	822	840	POTENTIAL.
FT	DOMAIN	841	871	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	872	892	POTENTIAL.
FT	DOMAIN	893	903	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	904	924	POTENTIAL.
FT	DOMAIN	925	941	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	942	958	POTENTIAL.
FT	DOMAIN	959	970	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	251	270	CALMODULIN-BINDING (POTENTIAL).
FT	REPEAT	138	178	ALPHA-1.
FT	REPEAT	407	478	BETA-1.
FT	REPEAT	539	609	BETA-2.
FT	REPEAT	839	875	ALPHA-2.
FT	DOMAIN	236	239	POLY-PHE.
FT	DOMAIN	689	692	POLY-GLU.
FT	DOMAIN	756	760	POLY-ASP.
FT	MOD_RES	389	389	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	866	866	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	970 AA;	108004 MW;	BBDBCC584846AE08 CRC64;

Query Match 66.9%; Score 2159.5; DB 1; Length 970;
 Best Local Similarity 69.9%; Pred. No. 2.6e-148;
 Matches 425; Conservative 73; Mismatches 89; Indels 21; Gaps 8;

Qy	1	MAWLRLQPLTSAFLHFGLVTFVLF--LNLRAEAGSGDVPSTGQNNESCSGSSDCKEGV	58
		: :: : : : : :	
Db	1	MLQLRLLPTFSMGCHLLAVVALLFSHVDLISAETEMEGEGNETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPN	118
		:: :: :: ::	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNM	178
		: :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFETAGDLGPSTIVGSAAFNM	176
Qy	179	FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQVWEGLLTL	238
		: :	
Db	177	FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVISPGVVEVWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH	295
		: : : :	
Db	237	FFFPICVVFVAVADRRLLFYKYVYKRYRAGKQRMIIIEHGEDRPSSKTEIEMDGKVVNSH	296
Qy	296	---FLDGNLVPLEGKEVD----ESRREMIRILKDLKQKHPEKDLDQLVEMANYYALSHQQ	348
		: : : : : : : : : : : : : : : : : : :	
Db	297	VDNFLDGALV-LEVDERDQDDEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ	355
Qy	349	KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSQC	407
		: :	
Db	356	KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTQC	415
Qy	408	LENCGAVLLTVVRKGGDMSKTMYVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG	467
		:: :	
Db	416	LENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKEPGETQKEIRVG	475

QY 468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
 |||||:| | |||:: | |:| | | | | ||| |||
 Db 476 IIDDDIFEEDENFLVHLSNVKVSSEASEDGILEANHVS---ALACLGSPSTATVTIFDDD 532

QY 528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
 ||||| | |||||:||||| |||||::|:||||:||||| |||
 Db 533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

QY 588 EFKNDETV 595
 ||:| | |
 Db 593 EFQNDEIV 600

RESULT 4

NAC1_FELCA

ID NAC1_FELCA STANDARD; PRT; 970 AA.
 AC P48767; P79174;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
 DE 1).
 GN SLC8A1 OR NCX1.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=96250114; PubMed=8659865;
 RA Menick D.R., Barnes K.V., Thacker U.F., Dawson M.M.,
 RA McDermott D.E., Rozich J.D., Kent R.L., Cooper G.;
 RT "The exchanger and cardiac hypertrophy."
 RL Ann. N.Y. Acad. Sci. 779:489-501(1996).
 RN [2]
 RP SEQUENCE OF 1-600 FROM N.A.
 RX MEDLINE=97269065; PubMed=9111065;
 RA Barnes K.V., Cheng G., Dawson M.M., Menick D.R.;
 RT "Cloning of cardiac, kidney, and brain promoters of the feline ncx1
 RT gene."
 RL J. Biol. Chem. 272:11510-11517(1997).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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CC -----
DR EMBL; L35846; AAB41941.1; -.
DR EMBL; U67075; AAB40148.1; -.
DR InterPro; IPR003644; Calx_beta.
DR InterPro; IPR004836; Na_Ca_Ex.
DR InterPro; IPR004837; NaCa_Exmemb.
DR Pfam; PF03160; Calx-beta; 2.
DR Pfam; PF01699; Na_Ca_Ex; 2.
DR PRINTS; PR01259; NACAEXCHNGR.
DR SMART; SM00237; Calx_beta; 2.
DR TIGRFAMs; TIGR00845; caca; 1.
KW Transport; Antiport; Calcium transport; Sodium transport;
KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
KW Calmodulin-binding; Repeat.
FT SIGNAL      1      32      POTENTIAL.
FT CHAIN       33     970     SODIUM/CALCIUM EXCHANGER 1.
FT DOMAIN      33      71     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM    72      93     POTENTIAL.
FT DOMAIN      94     133     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   134     155     POTENTIAL.
FT DOMAIN     156     167     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   168     188     POTENTIAL.
FT DOMAIN     189     199     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   200     222     POTENTIAL.
FT DOMAIN     223     225     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   226     249     POTENTIAL.
FT DOMAIN     250     769     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   770     789     POTENTIAL.
FT DOMAIN     790     796     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   797     819     POTENTIAL.
FT DOMAIN     820     821     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   822     840     POTENTIAL.
FT DOMAIN     841     871     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   872     892     POTENTIAL.
FT DOMAIN     893     903     CYTOPLASMIC (POTENTIAL).
FT TRANSMEM   904     924     POTENTIAL.
FT DOMAIN     925     941     EXTRACELLULAR (POTENTIAL).
FT TRANSMEM   942     958     POTENTIAL.
FT DOMAIN     959     970     CYTOPLASMIC (POTENTIAL).
FT DOMAIN    251     270     CALMODULIN-BINDING (POTENTIAL).
FT REPEAT     138     178     ALPHA-1.
FT REPEAT     407     478     BETA-1.
FT REPEAT     539     609     BETA-2.
FT REPEAT     839     875     ALPHA-2.
FT DOMAIN     236     239     POLY-PHE.
FT DOMAIN     689     692     POLY-GLU.
FT DOMAIN     756     760     POLY-ASP.
FT MOD_RES    389     389     PHOSPHORYLATION (POTENTIAL).
FT CARBOHYD    41      41     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD   157     157     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT    21      21     P -> A (IN REF. 2).
FT CONFLICT   113     113     K -> N (IN REF. 2).
SQ SEQUENCE   970 AA;  108004 MW;  2402F02DE35D4057 CRC64;

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Query Match          66.7%; Score 2152.5; DB 1; Length 970;
Best Local Similarity 70.0%; Pred. No. 8.2e-148;
Matches 426; Conservative 72; Mismatches 88; Indels 23; Gaps 10;

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=93037494; PubMed=1416984;
 RA Aceto J.F., Condrescu M., Kroupis C., Nelson H., Nelson N.,
 RA Nicoll D.A., Philipson K.D., Reeves J.P.;
 RT "Cloning and expression of the bovine cardiac sodium-calcium
 RT exchanger.";
 RL Arch. Biochem. Biophys. 298:553-560(1992).
 RN [2]
 RP SUBCELLULAR LOCATION.
 RC TISSUE=Retinal rod cell;
 RX MEDLINE=90241959; PubMed=2334719;
 RA Reid D.M., Friedel U., Molday R.S., Cook N.J.;
 RT "Identification of the sodium-calcium exchanger as the major
 RT ricin-binding glycoprotein of bovine rod outer segments and its
 RT localization to the plasma membrane.";
 RL Biochemistry 29:1601-1607(1990).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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 CC -----
 DR EMBL; L06438; AAA30509.1; -.
 DR PIR; S27114; S27114.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
 FT DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 POTENTIAL.
 FT DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).

FT	TRANSMEM	168	188	POTENTIAL.
FT	DOMAIN	189	199	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	200	222	POTENTIAL.
FT	DOMAIN	223	225	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	226	249	POTENTIAL.
FT	DOMAIN	250	769	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	770	789	POTENTIAL.
FT	DOMAIN	790	796	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	797	819	POTENTIAL.
FT	DOMAIN	820	821	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	822	840	POTENTIAL.
FT	DOMAIN	841	871	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	872	892	POTENTIAL.
FT	DOMAIN	893	903	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	904	924	POTENTIAL.
FT	DOMAIN	925	941	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	942	958	POTENTIAL.
FT	DOMAIN	959	970	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	251	270	CALMODULIN-BINDING (POTENTIAL).
FT	REPEAT	138	178	ALPHA-1.
FT	REPEAT	407	478	BETA-1.
FT	REPEAT	539	609	BETA-2.
FT	REPEAT	839	875	ALPHA-2.
FT	DOMAIN	236	239	POLY-PHE.
FT	DOMAIN	689	692	POLY-GLU.
FT	DOMAIN	756	760	POLY-ASP.
FT	MOD_RES	389	389	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	866	866	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	970 AA;	108027 MW;	7C29153D1F87DDBE CRC64;

Query Match 66.5%; Score 2147.5; DB 1; Length 970;
 Best Local Similarity 69.4%; Pred. No. 1.9e-147;
 Matches 422; Conservative 74; Mismatches 91; Indels 21; Gaps 8;

Qy	1	MAWLRLQPLTSAFLHFGVLTFVLF--LNLRAEAGGSGDVPSTGQNNESCSGSSDCKEGV	58
		: : : : : : :	
Db	1	MLQFSLSPTLSMGFHVIAVALLFSHVDHISAETEMEGEGNETGE----CTGSYYCKKGV	56
Qy	59	ILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIADRFTMASIEVITSQEREVTIKKPN	118
		: : : : : : : :	
Db	57	ILPIWEPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFTMSIEVITSQEKEITIKKPN	116
Qy	119	GETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAAGDLGPSTIVGSAAFNM	178
		: : : : : : : : :	
Db	117	GETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNM	176
Qy	179	FIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVVQWEGLLTL	238
		: : : : : :	
Db	177	FIIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTF	236
Qy	239	FFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIETEGDHPKG---IEMDGKMMNSH	295
		: : : : : : :	
Db	237	FFFPICVFAWVADRLLFYKYVYKRYRAGKQGRGMIIEHEDRPSSKTEIEMDGKVNSH	296
Qy	296	---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQLVEMANYYALSHQQ	348

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      |||| || || | | | :||| ||||:|||||||::||:|:| || ||
Db      297 VDSFLDGALV-LEVDERDQDDEEARREMARILKELKQKHPEKEIEQLIELANYQVLSQQQ 355

Qy      349 KSRAFYRIQATRMMTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQC 407
      ||||| |||||:|||||||:|:|:|:| || ||:|: | | :|:|:|: :|||
Db      356 KSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNTEVAENDPVSKIFFEQGTQC 415

Qy      408 LENC GAVLLTVVRKGGDSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVG 467
      ||||| | ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:| ||
Db      416 LENC GTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVVFKPGETQKEIRVG 475

Qy      468 IIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDD 527
      ||||| |||||:| | ||||:| | |:|: | | | | |||| |||
Db      476 IIDDDIFEEDENFLVHLSNVKVSLEASEDGILEASHVS---TLACLGSPSTATVTIFDDD 532

Qy      528 HAGIFTFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGEL 587
      ||||| |||||:||||||| ||||:|:|:|:| ||||| |||
Db      533 HAGIFTFEEPVTHVSESIGIMEVKVLRTSGARGNVIVPYKTIEGTARGGGEDFEDTCGEL 592

Qy      588 EFKNDETV 595
      ||:| || |
Db      593 EFQNDEIV 600

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RESULT 6

NAC1_HUMAN

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ID      NAC1_HUMAN      STANDARD;      PRT;      973 AA.
AC      P32418; O95849; Q9UBL8; Q9UDN1; Q9UDN2; Q9UKX6;
DT      01-OCT-1993 (Rel. 27, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      10-OCT-2003 (Rel. 42, Last annotation update)
DE      Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
DE      1).
GN      SLC8A1 OR NCX1 OR CNC.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORM 1).
RC      TISSUE=Heart;
RX      MEDLINE=92262521; PubMed=1374913;
RA      Komuro I., Wenninger K.E., Philipson K.D., Izumo S.;
RT      "Molecular cloning and characterization of the human cardiac Na+/Ca2+
RT      exchanger cDNA.";
RL      Proc. Natl. Acad. Sci. U.S.A. 89:4769-4773(1992).
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORMS 3 AND 7).
RX      MEDLINE=21136211; PubMed=11241183;
RA      Van Eylen F., Bollen A., Herchuelz A.;
RT      "NCX1 Na/Ca exchanger splice variants in pancreatic islet cells.";
RL      J. Endocrinol. 168:517-526(2001).
RN      [3]
RP      SEQUENCE FROM N.A. (ISOFORM 7).
RA      Mangini N.J., Chen W., Wang Q., Kennedy B.G.;
RT      "Na+/Ca2+ exchanger isoforms in cultured human retinal pigment
RT      epithelium.";

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RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE OF 1-603 FROM N.A.
 RA Rohlfing T., Strowmatt C., Scronce D., Moody T.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE OF 850-973 FROM N.A.
 RA Kozlowicz A., Stoneking T., Hawkins M., Le T.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
 RN [6]
 RP SEQUENCE OF 459-681 FROM N.A. (ISOFORM 10).
 RA Lundquist P., Lundgren T., Gritli-Linde A., Linde A.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1; Synonyms=NaCa1, NCX1.1;
 CC IsoId=P32418-1; Sequence=Displayed;
 CC Name=3; Synonyms=NaCa3, NCX1.3;
 CC IsoId=P32418-2; Sequence=VSP_003397, VSP_003398, VSP_003400;
 CC Name=7; Synonyms=NaCa7, NCX1.7;
 CC IsoId=P32418-3; Sequence=VSP_003397, VSP_003398, VSP_003399;
 CC Name=10; Synonyms=NaCa10, NCX1.10;
 CC IsoId=P32418-4; Sequence=VSP_003397, VSP_003398;
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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 CC -----
 DR EMBL; M91368; AAA35702.1; -.
 DR EMBL; AF108388; AAF08987.1; -.
 DR EMBL; AF108389; AAF08988.1; -.
 DR EMBL; AF128524; AAD26362.1; -.
 DR EMBL; AC007281; AAF19237.1; -.
 DR EMBL; AC007254; AAF19235.1; -.
 DR EMBL; AF115505; AAD17213.1; -.
 DR PIR; S32815; S32815.
 DR Genew; HGNC:11068; SLC8A1.
 DR MIM; 182305; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0015085; F:calcium ion transporter activity; TAS.
 DR GO; GO:0015081; F:sodium ion transporter activity; TAS.
 DR GO; GO:0006816; P:calcium ion transport; TAS.
 DR GO; GO:0006936; P:muscle contraction; TAS.
 DR GO; GO:0006814; P:sodium ion transport; TAS.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.

DR	InterPro; IPR004837; NaCa_Exmemb.			
DR	Pfam; PF03160; Calx-beta; 2.			
DR	Pfam; PF01699; Na_Ca_Ex; 2.			
DR	PRINTS; PR01259; NACAEXCHNGR.			
DR	SMART; SM00237; Calx_beta; 2.			
DR	TIGRFAMs; TIGR00845; caca; 1.			
KW	Transport; Antiport; Calcium transport; Sodium transport;			
KW	Transmembrane; Glycoprotein; Phosphorylation; Signal;			
KW	Calmodulin-binding; Repeat; Alternative splicing; Polymorphism.			
FT	SIGNAL	1	35	POTENTIAL.
FT	CHAIN	36	973	SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN	36	74	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	75	96	POTENTIAL.
FT	DOMAIN	97	136	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	137	158	POTENTIAL.
FT	DOMAIN	159	170	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	171	191	POTENTIAL.
FT	DOMAIN	192	202	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	203	225	POTENTIAL.
FT	DOMAIN	226	228	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	229	252	POTENTIAL.
FT	DOMAIN	253	772	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	773	792	POTENTIAL.
FT	DOMAIN	793	799	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	800	822	POTENTIAL.
FT	DOMAIN	823	824	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	825	843	POTENTIAL.
FT	DOMAIN	844	874	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	875	895	POTENTIAL.
FT	DOMAIN	896	906	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	907	927	POTENTIAL.
FT	DOMAIN	928	944	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	945	961	POTENTIAL.
FT	DOMAIN	962	973	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	254	273	CALMODULIN-BINDING (POTENTIAL).
FT	REPEAT	141	181	ALPHA-1.
FT	REPEAT	410	481	BETA-1.
FT	REPEAT	542	612	BETA-2.
FT	REPEAT	842	878	ALPHA-2.
FT	DOMAIN	239	242	POLY-PHE.
FT	DOMAIN	692	695	POLY-GLU.
FT	DOMAIN	759	763	POLY-ASP.
FT	MOD_RES	392	392	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	44	44	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	160	160	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	869	869	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	605	613	TISVKVIDD -> IITIRIFDR (in isoform 3,
FT				isoform 7 and isoform 10).
FT				/FTId=VSP_003397.
FT	VARSPPLIC	619	645	NKTFEIGEPRLVEMSEKKALLNEL -> ECSFSLVLEE
FT				PKWIRRGMK (in isoform 3, isoform 7 and
FT				isoform 10).
FT				/FTId=VSP_003398.
FT	VARSPPLIC	652	656	Missing (in isoform 7).
FT				/FTId=VSP_003399.
FT	VARSPPLIC	652	679	Missing (in isoform 3).
FT				/FTId=VSP_003400.

DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein
 DE 1).
 GN SLC8A1.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=95078257; PubMed=7986817;
 RA Tsuruya Y., Bersohn M.M., Li Z., Nicoll D.A., Philipson K.D.;
 RT "Molecular cloning and functional expression of the guinea pig
 RT cardiac Na(+)-Ca2+ exchanger.";
 RL Biochim. Biophys. Acta 1196:97-99(1994).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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 CC -----
 DR EMBL; U04955; AAA73904.1; -.
 DR PIR; I48097; I48097.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
 FT DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 POTENTIAL.
 FT DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 168 188 POTENTIAL.
 FT DOMAIN 189 199 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 200 222 POTENTIAL.
 FT DOMAIN 223 225 EXTRACELLULAR (POTENTIAL).

RN [4]
 RP TISSUE SPECIFICITY.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=96394663; PubMed=8798769;
 RA Nicoll D.A., Quednau B.D., Qui Z., Xia Y.-R., Lusis A.J.,
 RA Philipson K.D.;
 RT "Cloning of a third mammalian Na⁺-Ca²⁺ exchanger, NCX3."
 RL J. Biol. Chem. 271:24914-24921(1996).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=1; Synonyms=Heart, NaCa1;
 CC IsoId=Q01728-1; Sequence=Displayed;
 CC Name=2; Synonyms=Brain-1, NaCa5;
 CC IsoId=Q01728-2; Sequence=VSP_003402, VSP_003403;
 CC Name=3; Synonyms=Brain-2, NaCa4;
 CC IsoId=Q01728-3; Sequence=VSP_003402, VSP_003404;
 CC Name=4; Synonyms=Kidney-1, NaCa7;
 CC IsoId=Q01728-4; Sequence=VSP_003401, VSP_003402, VSP_003403;
 CC Name=5; Synonyms=Kidney-2, NaCa3;
 CC IsoId=Q01728-5; Sequence=VSP_003401, VSP_003402, VSP_003404;
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma or brain, and spleen.
 CC -----
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 CC -----
 DR EMBL; X68191; CAA48273.1; -.
 DR EMBL; X68812; CAA48707.1; -.
 DR EMBL; X68813; CAA48708.1; -.
 DR EMBL; U04933; AAB39952.1; -.
 DR EMBL; U04934; AAA19124.1; -.
 DR EMBL; U04936; AAA19125.1; -.
 DR PIR; A53789; A53789.
 DR PIR; S28833; S28833.
 DR PIR; S32435; S32435.
 DR PIR; S43730; S43730.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat; Alternative splicing.
 FT SIGNAL 1 32 POTENTIAL.

FT	CHAIN	33	971	SODIUM/CALCIUM EXCHANGER 1.
FT	DOMAIN	33	71	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	72	93	POTENTIAL.
FT	DOMAIN	94	133	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	134	155	POTENTIAL.
FT	DOMAIN	156	167	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	168	188	POTENTIAL.
FT	DOMAIN	189	199	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	200	222	POTENTIAL.
FT	DOMAIN	223	225	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	226	249	POTENTIAL.
FT	DOMAIN	250	770	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	771	790	POTENTIAL.
FT	DOMAIN	791	797	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	798	820	POTENTIAL.
FT	DOMAIN	821	822	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	823	841	POTENTIAL.
FT	DOMAIN	842	872	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	873	893	POTENTIAL.
FT	DOMAIN	894	904	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	905	925	POTENTIAL.
FT	DOMAIN	926	942	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	943	959	POTENTIAL.
FT	DOMAIN	960	971	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	251	270	CALMODULIN-BINDING (BY SIMILARITY).
FT	REPEAT	138	178	ALPHA-1.
FT	REPEAT	407	478	BETA-1.
FT	REPEAT	539	609	BETA-2.
FT	REPEAT	840	876	ALPHA-2.
FT	DOMAIN	236	239	POLY-PHE.
FT	DOMAIN	690	693	POLY-GLU.
FT	DOMAIN	757	761	POLY-ASP.
FT	MOD_RES	389	389	PHOSPHORYLATION (BY SIMILARITY).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	867	867	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	602	635	TISVKVIDDEEYEKKNKTFEIGEPRLVEMSEKK -> IIT
FT				IRIFDREEYEKECSFSLVLEEPKWIRRGMK (in
FT				isoform 4 and isoform 5).
FT				/FTid=VSP_003401.
FT	VARSPPLIC	636	642	Missing (in isoform 2, isoform 3, isoform
FT				4 and isoform 5).
FT				/FTid=VSP_003402.
FT	VARSPPLIC	649	654	Missing (in isoform 2 and isoform 4).
FT				/FTid=VSP_003403.
FT	VARSPPLIC	649	677	Missing (in isoform 3 and isoform 5).
FT				/FTid=VSP_003404.
FT	CONFLICT	250	250	D -> A (IN REF. 1).
FT	CONFLICT	402	402	P -> A (IN REF. 1).
SQ	SEQUENCE	971 AA;	108184 MW;	EC456CFE3AFC6A69 CRC64;

Query Match 66.2%; Score 2135.5; DB 1; Length 971;
 Best Local Similarity 68.8%; Pred. No. 1.4e-146;
 Matches 421; Conservative 72; Mismatches 86; Indels 33; Gaps 9;

Qy 4 LRLQPLTSAFLHFGVLTFVLEFL-----NGLRAEAGGSGDVPSTGQNNESCSCGSSDCK 55
 ||| : : | ||| | | || ||: |: || ||

Db 2 LRLSLPPNVSMGFRLVTLVALLFTHVDHITADTEAETGGN-----ETTECTGSYYCK 53

Qy 56 EGVILPIWYPENPSLGDKIARVIVYFVALIYMFLGVSIIADRFMASIEVITSQEREVTIK 115
:||||| |:| | ||||| |||||:|||||||:|||||||:|:|

Db 54 KGVILPIWEPQDPSEFGDKIARATVYFVAMVYMFVGVSIIADRFMSSIEVITSQEKEITIK 113

Qy 116 KPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEVCVGHGFIAGDLGPSTIVGSAA 175
|||||: |:|:|||||||:||||| | |||||

Db 114 KPNGETTKTTVRIWNETVSNLTLMALGSSAPEILLSVIEVCVGHNFTAGDLGPSTIVGSAA 173

Qy 176 FNMFIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLMLAVFSPGVVQVWEG 235
|||||: |:|:|||||||:||||||| ||:|:| ||||:||||

Db 174 FNMFIIALCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEG 233

Qy 236 LTLFFFFPVCVLLAWVADKRLLFYKYMHHKYRTDKHRGIIIEGTEGHPKG---IEMDGKMM 292
|| ||||:|: ||||:|:|:| | |:| | | | ||||:|

Db 234 LTLFFFFPICVVFVAVADRRLLFYKYVYKRYRAGKQGRMIIEHEGDRPASKTEIEMDGKV 293

Qy 293 NSH---FLDGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLDQLVEMANYALS 345
|| | ||| | | | | |:| | ||||:|:|:|:|:| | |

Db 294 NSHVDNFLDGLV-LEVDERDQDDEEARREMARILKELKQKHPDKEIEQLIELANYQVLS 352

Qy 346 HQQKSRAFYRIQATRMGTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCS 404
|||||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 353 QQQKSRAFYRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMDVVENDPVSKVFFEQGT 412

Qy 405 YQCLENCGAVLLTVVRKGGMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEF 464
||||||| | |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

Db 413 YQCLENCGTVALTIIRGGDLTNTVFVDFRTEDGTANAGSDYEFTEGTVIFKPGETQKEI 472

Qy 465 SVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPR-AVLASPCVATVTI 523
|||||||:| | ||||: | |:| | : | | | | |:|

Db 473 RVGIIDDDIFEEDENFLVHLSNVRSSEVSEEDG----ILDSNHVSAIACLGSPNTATITI 528

Qy 524 LDDDHAGIFTFECDTIHVSESIGVMEVKVLRITSGARGTVIVPFRTVEGTAKGGGEDFEDT 583
||||||| | |||||:|:|:|:|:|:|:|:|:|:|:|:|

Db 529 FDDDHAGIFTFEEPVTIVHSESIGIMEVKVLRITSGARGNVIIIPYKTIEGTARGGGGEDFEDT 588

Qy 584 YGELEFKNDETV 595
||||:| |

Db 589 CGELEFQNDIV 600

RESULT 9

NAC1_MOUSE

ID NAC1_MOUSE STANDARD; PRT; 970 AA.

AC P70414;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sodium/calcium exchanger 1 precursor (Na(+)/Ca(2+)-exchange protein

DE 1).

GN SLC8A1 OR NCX.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=96250070; PubMed=8659820;
 RA Kim I., Lee C.O.;
 RT "Cloning of the mouse cardiac Na(+)-Ca2+ exchanger and functional
 RT expression in Xenopus oocytes."
 RL Ann. N.Y. Acad. Sci. 779:126-128(1996).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Plasma membrane.
 CC -!- TISSUE SPECIFICITY: Cardiac sarcolemma.
 CC -----
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 CC -----
 DR EMBL; U70033; AAB46708.1; -.
 DR MGD; MGI:107956; Slc8a1.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 970 SODIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 33 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 93 POTENTIAL.
 FT DOMAIN 94 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 POTENTIAL.
 FT DOMAIN 156 167 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 168 188 POTENTIAL.
 FT DOMAIN 189 199 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 200 222 POTENTIAL.
 FT DOMAIN 223 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 249 POTENTIAL.
 FT DOMAIN 250 769 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 770 789 POTENTIAL.
 FT DOMAIN 790 796 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 797 819 POTENTIAL.
 FT DOMAIN 820 821 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 822 840 POTENTIAL.
 FT DOMAIN 841 871 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 872 892 POTENTIAL.
 FT DOMAIN 893 903 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	904	924	POTENTIAL.
FT	DOMAIN	925	941	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	942	958	POTENTIAL.
FT	DOMAIN	959	970	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	251	270	CALMODULIN-BINDING (POTENTIAL).
FT	REPEAT	138	178	ALPHA-1.
FT	REPEAT	407	478	BETA-1.
FT	REPEAT	539	609	BETA-2.
FT	REPEAT	839	875	ALPHA-2.
FT	DOMAIN	236	239	POLY-PHE.
FT	DOMAIN	689	692	POLY-GLU.
FT	DOMAIN	756	760	POLY-ASP.
FT	MOD_RES	389	389	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	41	41	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	157	157	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	866	866	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	970 AA;	108035 MW;	F5FC0BD07F2B6602 CRC64;

Query Match 65.5%; Score 2115.5; DB 1; Length 970;
 Best Local Similarity 68.3%; Pred. No. 3.9e-145;
 Matches 412; Conservative 76; Mismatches 100; Indels 15; Gaps 6;

Qy	4	LRLQPLTSAFLHFGVLTVFLFLNGLRAEAGGSGDVPSTGQNNESCSGSSDCKEGVILPIW	63
		: : : : : :	
Db	2	LRLSLPPNVSMGFRLVALVALLFSHVDHITADTEAETGGNETTECTGSYYCKKGVLPIW	61
Qy	64	YPENPSLGDKIARVIVYFVALIYMFLGVSIADRFMASIEVITSQEREVTIKKPNGETST	123
		:: :: :: ::	
Db	62	EPQDPSFGDKIARATVYFVAMVYMFLGVSIADRFMSSIEVITSQEKEITIKKPNGETTK	121
Qy	124	TTIRVWNETVSNLTLMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIG	183
		: : : : :	
Db	122	TTVRIWNETVSNLTLMALGSSAPEILLSVIEVCGHNFTAGDLGPSTIVGSAAFNMFIIA	181
Qy	184	ICVYVIPDGETRRIKHLRVFFITAAWSIFAYIWLYMILAVFSPGVQVWEGLLTLFFFPV	243
		: : : : : : :	
Db	182	LCVYVVPDGETRRIKHLRVFFVTAAWSIFAYTWLYIILSVSSPGVVEVWEGLLTFFFFP	241
Qy	244	CVLLAWVADKRLLFYKYMHHKYRTDKHRGIIETEGDHPKG---IEMDGKMMNSH---FL	297
		: : : : : :	
Db	242	CVVFAWVADRRLLFYKYVKRYRAGKQGMIIIEHGEDRPASKTEIEMDGKVNSHVDNFL	301
Qy	298	DGNLVPLEGKEVD---ESRREMIRILKDLKQKHPEKDLQVLVEMANYALSHQQKSRAF	353
		: : : : :	
Db	302	DGALV-LEVDERDQDDEEARREMARILKELQKHPEKEIEQLIELANYQVLSQQQKSRAF	360
Qy	354	YRIQATRMGTGAGNILKKHAAEQAKKASSMSEVHTDEPE-DFISKVFFDPCSYQCLENCG	412
		: : : : : : : : : :	
Db	361	YRIQATRLMTGAGNILKRHAADQARKAVSMHEVNMEMAENDPVSKIFFEQGTQYQCLENCG	420
Qy	413	AVLLTVVRKGGMSKTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDD	472
		: : : : : : :	
Db	421	TVALTIMRRGGDLSTTVFVDFRTEDGTANAASDYEFTEGTVIFKPGETQKEIRVGIIDDD	480
Qy	473	IFEEDHFFVRLSNVRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIF	532
		: : : : :	
Db	481	IFEEDENFLVHLSNVRVSSDVSEDGI---LESNHASSIACLGSPSTATITIFDDDHAGIF	537

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Qy      533 TFECDTIHVSESIGVMEVKVLRTSGARGTVIVPFRTVEGTAKGGGEDFEDTYGELEFKND 592
      ||| |||||:||||||| ||:|::|:||||| || ||:|
Db      538 TFEEPVTHVSESIGIMEVKVLRTSGARGNVIIPYKTIEGTARGGGEDFEDTCGEPEFQND 597

Qy      593 ETV 595
      | |
Db      598 EIV 600

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RESULT 10

NAC2_HUMAN

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ID      NAC2_HUMAN      STANDARD;      PRT;      921 AA.
AC      Q9UPR5;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Sodium/calcium exchanger 2 precursor (Na(+)/Ca(2+)-exchange protein
DE      2).
GN      SLC8A2 OR NCX2 OR KIAA1087.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=99397452; PubMed=10470851;
RA      Kikuno R., Nagase T., Ishikawa K.-I., Hirose M., Miyajima N.,
RA      Tanaka A., Kotani H., Nomura N., Ohara O.;
RT      "Prediction of the coding sequences of unidentified human genes. XIV.
RT      The complete sequences of 100 new cDNA clones from brain which code
RT      for large proteins in vitro.";
RL      DNA Res. 6:197-205(1999).
CC      -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
CC      coupling. Ca(2+) is extruded from the cell during relaxation so as
CC      to prevent overloading of intracellular stores (By similarity).
CC      -!- ENZYME REGULATION: By ATP (By similarity).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -----
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CC      -----
DR      EMBL; AB029010; BAA83039.1; ALT_INIT.
DR      Genew; HGNC:11069; SLC8A2.
DR      MIM; 601901; -.
DR      InterPro; IPR003644; Calx_beta.
DR      InterPro; IPR004836; Na_Ca_Ex.
DR      InterPro; IPR004837; NaCa_Exmemb.
DR      Pfam; PF03160; Calx-beta; 2.
DR      Pfam; PF01699; Na_Ca_Ex; 2.
DR      PRINTS; PR01259; NACAEXCHNGR.

```


RA Philipson K.D.;
 RT "Cloning of a third mammalian Na⁺-Ca²⁺ exchanger, NCX3.";
 RL J. Biol. Chem. 271:24914-24921(1996).
 CC -!- FUNCTION: Rapidly transports Ca(2+) during excitation-contraction
 CC coupling. Ca(2+) is extruded from the cell during relaxation so as
 CC to prevent overloading of intracellular stores.
 CC -!- ENZYME REGULATION: By ATP.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Brain and skeletal muscle.
 CC -----
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 CC -----
 DR EMBL; U08141; AAA19920.1; -.
 DR PIR; A54139; A54139.
 DR InterPro; IPR003644; Calx_beta.
 DR InterPro; IPR004836; Na_Ca_Ex.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF03160; Calx-beta; 2.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR PRINTS; PR01259; NACAEXCHNGR.
 DR SMART; SM00237; Calx_beta; 2.
 DR TIGRFAMs; TIGR00845; caca; 1.
 KW Transport; Antiport; Calcium transport; Sodium transport;
 KW Transmembrane; Glycoprotein; Phosphorylation; Signal;
 KW Calmodulin-binding; Repeat.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 921 SODIUM/CALCIUM EXCHANGER 2.
 FT DOMAIN 21 68 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 69 90 POTENTIAL.
 FT DOMAIN 91 130 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 131 152 POTENTIAL.
 FT DOMAIN 153 164 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 165 185 POTENTIAL.
 FT DOMAIN 186 196 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 197 219 POTENTIAL.
 FT DOMAIN 220 222 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 223 246 POTENTIAL.
 FT DOMAIN 247 720 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 721 740 POTENTIAL.
 FT DOMAIN 741 747 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 748 770 POTENTIAL.
 FT DOMAIN 771 772 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 773 791 POTENTIAL.
 FT DOMAIN 792 822 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 823 843 POTENTIAL.
 FT DOMAIN 844 854 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 855 875 POTENTIAL.
 FT DOMAIN 876 892 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 893 909 POTENTIAL.
 FT DOMAIN 910 921 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 248 267 CALMODULIN-BINDING (BY SIMILARITY).

Query Match 60.5%; Score 1954.5; DB 1; Length 921;
Best Local Similarity 64.1%; Pred. No. 1.6e-133;
Matches 371; Conservative 92; Mismatches 91; Indels 25; Gaps 6;

[illegible]

RESULT 12
NKX1 CHICK

ID NKX1_CHICK STANDARD; PRT; 663 AA.
 AC Q9IAL8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-
 DE exchange protein 1) (Retinal rod Na-Ca+K exchanger).
 GN SLC24A1 OR NCKX1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=20130359; PubMed=10662833;
 RA Prinsen C.F.M., Szerencsei R.T., Schnetkamp P.P.M.;
 RT "Molecular cloning and functional expression of the potassium-
 RT dependent sodium-calcium exchanger from human and chicken retinal cone
 RT photoreceptors.";
 RL J. Neurosci. 20:1424-1434(2000).
 CC -!- FUNCTION: Critical component of the visual transduction cascade,
 CC controlling the calcium concentration of outer segments during
 CC light and darkness. Light causes a rapid lowering of cytosolic
 CC free calcium in the outer segment of both retinal rod and cone
 CC photoreceptors and the light-induced lowering of calcium is caused
 CC by extrusion via this protein which plays a key role in the
 CC process of light adaptation. Transports one Ca(2+) and one K(+) in
 CC exchange for four Na(+).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Retinal rods. Localizes to the inner segment
 CC of rod photoreceptors.
 CC -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
 CC -----
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 CC -----
 DR EMBL; AF177984; AAF25808.1; -.
 DR InterPro; IPR004817; K_NaCaexchang.
 DR InterPro; IPR004481; K_NaCaexchnng.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR TIGRFAMs; TIGR00927; 2A1904; 1.
 DR TIGRFAMs; TIGR00367; TIGR00367; 1.
 KW Vision; Transport; Antiport; Symport; Calcium transport;
 KW Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
 KW Phosphorylation; Signal; Repeat.
 FT SIGNAL 1 31 POTENTIAL.
 FT CHAIN 32 663 SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
 FT DOMAIN 32 128 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 129 149 POTENTIAL.

FT	DOMAIN	150	173	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	174	194	POTENTIAL.
FT	DOMAIN	195	200	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	201	221	POTENTIAL.
FT	DOMAIN	222	228	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	229	253	POTENTIAL.
FT	DOMAIN	254	259	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	260	276	POTENTIAL.
FT	DOMAIN	277	471	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	472	492	POTENTIAL.
FT	DOMAIN	493	499	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	500	520	POTENTIAL.
FT	DOMAIN	521	535	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	536	556	POTENTIAL.
FT	DOMAIN	557	574	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	575	595	POTENTIAL.
FT	DOMAIN	596	604	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	605	625	POTENTIAL.
FT	DOMAIN	626	632	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	633	653	POTENTIAL.
FT	DOMAIN	654	663	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	170	210	ALPHA-1.
FT	REPEAT	543	574	ALPHA-2.
FT	MOD_RES	337	337	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	59	59	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	66	66	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	100	100	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	663 AA; 73771 MW; DD624E3080C43082 CRC64;		

Query Match 6.5%; Score 209.5; DB 1; Length 663;
 Best Local Similarity 21.9%; Pred. No. 2.1e-07;
 Matches 124; Conservative 74; Mismatches 166; Indels 203; Gaps 26;

Qy	77	VIVYFVALIYMFLGVSIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN	135
		::: :: :: : :: : :: :: :	::: : :
Db	131	VVLHIFGMMYVFVALAIVCDEYFVPALGVITEK-----LQI-SEDVAG	172
Qy	136	LTLMALGSSAPEILLSLIEVCGHGFA-GDLGPSTIVGSAAFNMFIIGICVYVIPDGET	194
		: : :: : : :	
Db	173	ATFMAAGGSAPELFTSLIGV----FISHSNVGIGTIVGSAVFNILFVIGTCALF-----S	223
Qy	195	RKIKHLRVFFITAAWSIFAYIWLY-----MILAVFSPGVVQVWEGLLTLFFFPVCV----	245
		: : :: : :	
Db	224	REILHL-----TWWPLFRDISFYIVDLLMLILFFLDSDVIDWWESLLLLTAYATYVFTMK	277
Qy	246	----LLAWVADK-----RLLFYKYMHHKYRTDKHRGIIIIETEGDHPKGIEMDGKMM-	292
		:: : : : : : :	
Db	278	HNVSLEQWVKEELSKKLNVAQAASAEHMRKK-----SSVAVAEDGTPK----ADGKKLQ	327
Qy	293	-----NS-----HFLDGNLVPLEGKEVDESRRREMIRILKDLKQK	326
		: : : :: :	
Db	328	PTTALQRGTTSSASLHNSQMRSTIFQLMIHTLD----PLAGAKF----KDRV DILSNI AKV	379
Qy	327	HPEKDL DQLVEMANYYALSHQQKSRAF YRIQATRMMTGAGN ILKKHAAEQAKKASSMSEV	386
		: : ::	
Db	380	KADS-----LTGQGT---KPEAE E E KQASQ----	401

```

Qy      387 HTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGMSKTMVVDYKTEDGSANAGADY 446
          : | | | : || : :| : :|
Db      402 -----NTVQVTPAS-----DSEPSKDKQKEDTPQDGQPPSDSD- 434

Qy      447 EFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSNVRIEEEQPEEGMPPAIFNSL 506
          | | | | : :| : : | | | : |
Db      435 -----NSEDSSSDSEDDSDDDSTDDEE-----NDEPLSLEWPETRKKQAIYLF 478

Qy      507 PLPRAVLASPCVATVTIL---DDDHAGIFTFECDTI-----HVSESIGVME 549
          | : | :| : | : || | | :| :|
Db      479 -FP---IVFPLWSTIPDVRNPDSKKFFVITFFGSIIWIAAFSYLMVWWAHQVGETIGISE 534

Qy      550 VKVLRTSGARGTVIVPFRTVEGTAKGG 576
          : | | | | | : |
Db      535 EIMGLTILAAGTSIPDLITSVIVARKG 561

```

RESULT 13

NKX2_HUMAN

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ID      NKX2_HUMAN      STANDARD;      PRT;      661 AA.
AC      Q9UI40; Q9NTN5; Q9NZQ4;
DT      28-FEB-2003 (Rel. 41, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Sodium/potassium/calcium exchanger 2 precursor (Na(+)/K(+)/Ca(2+)-
DE      exchange protein 2) (Retinal cone Na-Ca+K exchanger).
GN      SLC24A2 OR NCKX2.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC      TISSUE=Retina;
RX      MEDLINE=20130359; PubMed=10662833;
RA      Prinsen C.F.M., Szerencsei R.T., Schnetkamp P.P.M.;
RT      "Molecular cloning and functional expression of the potassium-
RT      dependent sodium-calcium exchanger from human and chicken retinal cone
RT      photoreceptors.";
RL      J. Neurosci. 20:1424-1434(2000).
RN      [2]
RP      SEQUENCE OF 311-376 FROM N.A. (ISOFORM 1).
RA      Sehra H.;
RL      Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
CC      -!- FUNCTION: Critical component of the visual transduction cascade,
CC      controlling the calcium concentration of outer segments during
CC      light and darkness. Light causes a rapid lowering of cytosolic
CC      free calcium in the outer segment of both retinal rod and cone
CC      photoreceptors and the light-induced lowering of calcium is caused
CC      by extrusion via this protein which plays a key role in the
CC      process of light adaptation. Transports one Ca(2+) and one K(+) in
CC      exchange for four Na(+).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -!- ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=2;
CC      Name=1;
CC      IsoId=Q9UI40-1; Sequence=Displayed;

```

```

CC      Name=2;
CC      IsoId=Q9UI40-2; Sequence=VSP_006164;
CC      -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF097366; AAF21810.1; -.
DR      EMBL; AF177987; AAF25811.1; -.
DR      EMBL; AL133281; CAB92751.2; -.
DR      Genew; HGNC:10976; SLC24A2.
DR      InterPro; IPR004481; K_NaCaexchnng.
DR      InterPro; IPR004837; NaCa_Exmemb.
DR      Pfam; PF01699; Na_Ca_Ex; 2.
DR      TIGRFAMs; TIGR00367; TIGR00367; 1.
KW      Vision; Transport; Antiport; Symport; Calcium transport;
KW      Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
KW      Signal; Repeat; Alternative splicing.
FT      SIGNAL      1      58      POTENTIAL.
FT      CHAIN      59      661      SODIUM/POTASSIUM/CALCIUM EXCHANGER 2.
FT      DOMAIN      59      132      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      133      153      POTENTIAL.
FT      DOMAIN      154      178      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      179      199      POTENTIAL.
FT      DOMAIN      200      204      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      205      225      POTENTIAL.
FT      DOMAIN      226      243      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      244      264      POTENTIAL.
FT      DOMAIN      265      265      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      266      286      POTENTIAL.
FT      DOMAIN      287      469      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      470      490      POTENTIAL.
FT      DOMAIN      491      497      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      498      518      POTENTIAL.
FT      DOMAIN      519      533      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      534      554      POTENTIAL.
FT      DOMAIN      555      569      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      570      590      POTENTIAL.
FT      DOMAIN      591      602      CYTOPLASMIC (POTENTIAL).
FT      TRANSMEM      603      623      POTENTIAL.
FT      DOMAIN      624      630      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      631      651      POTENTIAL.
FT      DOMAIN      652      661      CYTOPLASMIC (POTENTIAL).
FT      REPEAT      174      214      ALPHA-1.
FT      REPEAT      541      572      ALPHA-2.
FT      CARBOHYD      111      111      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      VARSPLIC      360      376      Missing (in isoform 2).
FT                                          /FTId=VSP_006164.
SQ      SEQUENCE      661 AA; 73663 MW; E6359C1F95C3AB3E CRC64;

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Query Match          6.3%; Score 203.5; DB 1; Length 661;
Best Local Similarity 22.3%; Pred. No. 5.6e-07;

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Matches 128; Conservative 91; Mismatches 204; Indels 151; Gaps 28;

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Qy      39 PSTGQNNESCSGSSDCKEGVILPIWYPENP-SLGD-KIARVIVYFVALIYMFLGVSIIAD 96
      | : || | :| :| ||:: || : : :|:: : :|||: :|: |
Db     101 PPLSKEGES-ENSTDHAQGD-----YPKDIFSLEERRKGAILLHVIGMIYMFIALAIVCD 154

Qy      97 R-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEV 155
      |: |: ||| : : : :|: | || | ||||: ||| |
Db     155 EFFVPSLTVITEK-----LGI-SDDVAGATFMAAGGSAPELFTSLIGV 196

Qy     156 CGHGFIAGDLGPSTIVGSAAENMFIIIGICVYVIPDGETRRIKHLRVFFITAAWSIFAY 214
      ||| :| ||||| ||: :||:| :|:| :| :| :|
Db     197 ----FIAHSNVGIGTIVGSAVFNILEFVIGMCALF-----SREILNL-----TWWPLFRD 241

Qy     215 IWLY-----MILAVFSPGVVQWEGLLTL-FFFPVCVLL-----AWVADKRLLFYKYM 261
      : | |:: | | : || || | :| | : || |:: :
Db     242 VSFYIVDLIMLIIFFLDNVIMWWESLLLLLTAYFCYVFMKFNQVEKWV--KQMINRNKV 299

Qy     262 HKKYRTDKHRGIIIETEGDHP-----KGIEMDGKMMNSH--FLDGNLVPLEGKEVDESRR 314
      | : : | | : : | : | : : |
Db     300 VKVTAPEAQAKPSAARDKDEPTLPKPRQLQGGSSASLHNSLMRNSIFQL----- 349

Qy     315 EMIRILKDLKQKHPEKDLDQLVEMANYYALSHQOKSRAFYRIQATRMMTGAGNILKKHAA 374
      || | | : | : | | : || | :| :
Db     350 -MIHTLDPLAE-----ELGSYGKLYYD-----TMTEEGRFREKASI 385

Qy     375 --EQAKKASSMSEVHTDEPE-----DFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMS 426
      : ||| : | || | : : | : : : :| : : :|::|
Db     386 LHKIAKK-----KCHVDENERQNGAANHVEKIELPNSTSTDVEMTPSSDASEPVQNGNLS 440

Qy     427 KTMVVDYKTEDGSANAGADYEFTEGTVVLKPGETQKEFSVGIIDDDIFEDEHFFVRLSN 486
      : :|: || | : : | ||: : : | : :| : :
Db     441 HNI-----EGAEAQTADEEDQPLSLAWPSETRKQVTFLIVFPIVFP----LWITLPD 489

Qy     487 VRIEEEQPEEGMPPAIFNSLPLPRAVLASPCVATVTILDDDHAGIFTFECDTI----HVS 542
      || : : | | : | : | : | : | : |
Db     490 VR--KPSSRKFFPITFFGSI-----TWIAVFSYLMVWWAHQVG 525

Qy     543 ESIGVMEVKVLRRTSGARGTVIVPFRTVEGTAKGG 576
      |:|: | : | || | | : |
Db     526 ETIGISEEIMGLTILAAGTSIPDLITSVIVARKG 559

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RESULT 14

NKX1_RAT

ID NKX1_RAT STANDARD; PRT; 1181 AA.

AC Q9QZM6; Q62932;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sodium/potassium/calcium exchanger 1 precursor (Na(+)/K(+)/Ca(2+)-

DE exchange protein 1) (Retinal rod Na-Ca+K exchanger).

GN SLC24A1 OR NCKX1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

```

RN      [1]
RP      SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC      STRAIN=Sprague-Dawley; TISSUE=Eye;
RX      MEDLINE=20217335; PubMed=10751314;
RA      Poon S., Leach S., Li X.-F., Tucker J.E., Schnetkamp P.P.M.,
RA      Lytton J.;
RT      "Alternatively spliced isoforms of the rat eye
RT      sodium/calcium+potassium exchanger NCKX1.";
RL      Am. J. Physiol. 278:C651-C660(2000).
RN      [2]
RP      SEQUENCE OF 1067-1155 FROM N.A.
RA      White K.E., Gesek F.A., Friedman P.A.;
RL      Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
CC      -!- FUNCTION: Critical component of the visual transduction cascade,
CC      controlling the calcium concentration of outer segments during
CC      light and darkness. Light causes a rapid lowering of cytosolic
CC      free calcium in the outer segment of both retinal rod and cone
CC      photoreceptors and the light-induced lowering of calcium is caused
CC      by extrusion via this protein which plays a key role in the
CC      process of light adaptation. Transports one Ca(2+) and one K(+) in
CC      exchange for four Na(+).
CC      -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=4;
CC          Name=1;
CC              IsoId=Q9QZM6-1; Sequence=Displayed;
CC          Name=2;
CC              IsoId=Q9QZM6-2; Sequence=VSP_006161;
CC          Name=3;
CC              IsoId=Q9QZM6-3; Sequence=VSP_006162;
CC          Name=4;
CC              IsoId=Q9QZM6-4; Sequence=VSP_006163;
CC      -!- TISSUE SPECIFICITY: Highly expressed in the eye.
CC      -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF176688; AAD53121.1; -.
DR      EMBL; U49235; AAB37753.1; -.
DR      InterPro; IPR004817; K_NaCaexchang.
DR      InterPro; IPR004481; K_NaCaexchnng.
DR      InterPro; IPR004837; NaCa_Exmemb.
DR      Pfam; PF01699; Na_Ca_Ex; 2.
DR      TIGRFAMs; TIGR00927; 2A1904; 1.
DR      TIGRFAMs; TIGR00367; TIGR00367; 1.
KW      Vision; Transport; Antiport; Symport; Calcium transport;
KW      Transmembrane; Glycoprotein; Phosphorylation; Signal; Repeat;
KW      Alternative splicing.
FT      SIGNAL          1      38      POTENTIAL.
FT      CHAIN           39     1181     SODIUM/POTASSIUM/CALCIUM EXCHANGER 1.
FT      DOMAIN          39      419     EXTRACELLULAR (POTENTIAL).

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FT	TRANSMEM	420	440	POTENTIAL.
FT	DOMAIN	441	464	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	465	485	POTENTIAL.
FT	DOMAIN	486	491	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	492	512	POTENTIAL.
FT	DOMAIN	513	519	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	520	544	POTENTIAL.
FT	DOMAIN	545	552	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	553	569	POTENTIAL.
FT	DOMAIN	570	989	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	990	1010	POTENTIAL.
FT	DOMAIN	1011	1017	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1018	1038	POTENTIAL.
FT	DOMAIN	1039	1053	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1054	1074	POTENTIAL.
FT	DOMAIN	1075	1092	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1093	1113	POTENTIAL.
FT	DOMAIN	1114	1121	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	1122	1142	POTENTIAL.
FT	DOMAIN	1143	1150	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1151	1171	POTENTIAL.
FT	DOMAIN	1172	1181	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	461	501	ALPHA-1.
FT	REPEAT	1061	1092	ALPHA-2.
FT	DOMAIN	730	905	14 X APPROXIMATE TANDEM REPEATS.
FT	REPEAT	730	741	1.
FT	REPEAT	742	754	2.
FT	REPEAT	755	766	3.
FT	REPEAT	767	778	4.
FT	REPEAT	779	791	5.
FT	REPEAT	792	804	6.
FT	REPEAT	805	817	7.
FT	REPEAT	818	830	8.
FT	REPEAT	831	843	9.
FT	REPEAT	844	856	10.
FT	REPEAT	857	869	11.
FT	REPEAT	870	881	12.
FT	REPEAT	882	893	13.
FT	REPEAT	894	905	14.
FT	DOMAIN	952	974	POLY-GLU.
FT	MOD_RES	625	625	PHOSPHORYLATION (POTENTIAL).
FT	CARBOHYD	271	271	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	598	710	Missing (in isoform 2).
FT				/FTId=VSP_006161.
FT	VARSPLIC	616	710	Missing (in isoform 3).
FT				/FTId=VSP_006162.
FT	VARSPLIC	652	679	Missing (in isoform 4).
FT				/FTId=VSP_006163.
SQ	SEQUENCE	1181 AA;	129980 MW;	B063C1C1193696AE CRC64;

Query Match 6.3%; Score 203; DB 1; Length 1181;
 Best Local Similarity 20.7%; Pred. No. 1.3e-06;
 Matches 134; Conservative 89; Mismatches 207; Indels 216; Gaps 29;

Qy	77	VIVYFVALIYMFLGVSIIADR-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSN	135
		::: : : : :: : : :: : :: : :	
Db	422	VVLHIFGMTYVFVALAIVCDEYFVPALGVITDK-----LQI-SEDVAG	463

Qy 136 LTIMALGSSAPEILLSLIEVCGHGFIAGDLGPSTIVGSAAFNMFIIIGICVYVIPDGET 194
 | | | | | | : | | | | | : : | | | | | : : | | :
 Db 464 ATFMAAGGSAPLEFTSLIGV----FISHSNVGIGTIVGSAVFNILFVIGTCALF-----S 514

Qy 195 RKIKHLRVFFITAAWSIFAYIWLY-----MILAVFSPGVVQVWEGLLTLFFFPVCV----- 245
 | : | : | | : | : | | : | : | | | : : |
 Db 515 REILNL-----TWWPLFRDVSEFYILDLSMLIVFFLDLSLIAWWESLLLLLAYALYVFTMK 568

Qy 246 ----LLAWVADK--RLLFYKYMHHKYRTDKHRGIIETEGDHPKGIEM-----DGK 290
 : | | : : | | : | | | | : : :
 Db 569 WNKQIERWVKEQLSRPVAKVMAIGDLSKPSDGAIEENEQQDNKKLKLPSVLTRGSSSSAS 628

Qy 291 MMNS-----HFLDGNLVPL----EGKEVDESRRMIRILKDLK-----QKHP----- 328
 : | | : : | | : | | : | | : : |
 Db 629 LHSNIIRSTIYHMLHSLDPLGEARPSKDKQESLNQEARVLPQTKAESSSDEEEPAELPA 688

Qy 329 -----EKDLDQLVEMANYIALSHQQKSRAFYRIQATRMMTGAGN 367
 : : | : : : : : : : : :
 Db 689 VTVTPAPAPEDKGDQEEDEPGCQEDVDEAEHRGDMTGEEGERETEA----EGKKDEEGETE 744

Qy 368 ILKKHAAEQAKKASSMSEVHTDEPEDFISKVFFDPCSYQCLENCGAVLLTVVRKGGDMSK 427
 : | : : : : | | : | | : | |
 Db 745 AERKEDGQEEETETKQKEKQEGETES-----EGKD----- 774

Qy 428 TMYVDYKTEDGSANAGADYE---FTEGTVVLKPGETQKEFSVGIIDDDIFE----- 475
 : : | : | : | | | | | : | : |
 Db 775 ----EQEGETEAEKGADHEGETEAEGKEVEHEGETEAEG---GTEDEQEGETEAEGKEVE 827

Qy 476 -----EDEHFFVRLSNVRIEEEQPE---EGMPPAIFNSLPLPRAVLASPCVATVT 522
 | | | | | : | | | |
 Db 828 QEGETEAEGKEVEH-----EVETEAEKRNHEGETEAEGK----- 863

Qy 523 ILDDDHAGIFTFECDTIH--VSESIGVMEVKVLRVTSARGTVIVPFRTVEGTAKGGGEDF 580
 : | | | : | : | : | : : : : | : : |
 Db 864 --EADHEGETEAEGNVEHQGETEAEGKVEHEGETEAEGKD-----EHEGQSETQADDT 914

Qy 581 E--DTYGELEFKNDETVCDRQEADYGRRG-----QEDSRD 614
 | | | | | : : : | | : | |
 Db 915 EVKDGEAE-ANAEDQCETAQGEKGADGGGSDGGDSEEEDEED 959

RESULT 15

NKX2_RAT

ID NKX2_RAT STANDARD; PRT; 670 AA.

AC O54701; O54706;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Sodium/potassium/calcium exchanger 2 precursor (Na(+)/K(+)/Ca(2+)-exchange protein 2) (Retinal cone Na-Ca+K exchanger).

GN SLC24A2 OR NKX2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
 RX MEDLINE=98129830; PubMed=9461611;
 RA Tsoi M., Rhee K.-H., Bungard D., Li X.-F., Lee S.-L., Auer R.N.,
 RA Lytton J.;
 RT "Molecular cloning of a novel potassium-dependent sodium-calcium
 RT exchanger from rat brain.";
 RL J. Biol. Chem. 273:4155-4162(1998).
 CC -!- FUNCTION: Critical component of the visual transduction cascade,
 CC controlling the calcium concentration of outer segments during
 CC light and darkness. Light causes a rapid lowering of cytosolic
 CC free calcium in the outer segment of both retinal rod and cone
 CC photoreceptors and the light-induced lowering of calcium is caused
 CC by extrusion via this protein which plays a key role in the
 CC process of light adaptation. Transports one Ca(2+) and one K(+) in
 CC exchange for four Na(+).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=O54701-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=O54701-2; Sequence=VSP_006165;
 CC -!- TISSUE SPECIFICITY: Expressed abundantly in all regions of the
 CC brain and weakly in the eye, large intestine and adrenal tissue.
 CC -!- SIMILARITY: BELONGS TO THE SLC24A FAMILY OF TRANSPORTERS.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF021923; AAC19405.1; -.
 DR EMBL; AF027506; AAC19404.1; -.
 DR InterPro; IPR004481; K_NaCaexchg.
 DR InterPro; IPR004837; NaCa_Exmemb.
 DR Pfam; PF01699; Na_Ca_Ex; 2.
 DR TIGRFAMs; TIGR00367; TIGR00367; 1.
 KW Vision; Transport; Antiport; Symport; Calcium transport;
 KW Potassium transport; Sodium transport; Transmembrane; Glycoprotein;
 KW Signal; Repeat; Alternative splicing.
 FT SIGNAL 1 58 POTENTIAL.
 FT CHAIN 59 670 SODIUM/POTASSIUM/CALCIUM EXCHANGER 2.
 FT DOMAIN 59 133 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 134 154 POTENTIAL.
 FT DOMAIN 155 179 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 180 200 POTENTIAL.
 FT DOMAIN 201 205 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 206 226 POTENTIAL.
 FT DOMAIN 227 244 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 245 265 POTENTIAL.
 FT DOMAIN 266 266 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 267 287 POTENTIAL.
 FT DOMAIN 288 478 CYTOPLASMIC (POTENTIAL).

FT	TRANSMEM	479	499	POTENTIAL.
FT	DOMAIN	500	506	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	507	527	POTENTIAL.
FT	DOMAIN	528	542	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	543	563	POTENTIAL.
FT	DOMAIN	564	578	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	579	599	POTENTIAL.
FT	DOMAIN	600	611	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	612	632	POTENTIAL.
FT	DOMAIN	633	639	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	640	660	POTENTIAL.
FT	DOMAIN	661	670	CYTOPLASMIC (POTENTIAL).
FT	REPEAT	175	215	ALPHA-1.
FT	REPEAT	550	581	ALPHA-2.
FT	CARBOHYD	112	112	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	360	376	Missing (in isoform 2).
FT				/FTid=VSP_006165.
FT	CONFLICT	309	309	Q -> R (IN REF. 1; AAC19404).
SQ	SEQUENCE	670 AA;	74656 MW;	4E855A467FC6679E CRC64;

Query Match 6.2%; Score 201.5; DB 1; Length 670;
 Best Local Similarity 24.2%; Pred. No. 7.9e-07;
 Matches 102; Conservative 67; Mismatches 128; Indels 125; Gaps 25;

Qy	39	PSTGQNNESCSGSSDCKE	GVLPIWYPENP-SLGD-KIARVIVYFVALIYMFLGVSIIAD	96
		: : :	:: : : : :: : : : : :	
Db	102	PPASQEDRSENG-TDHAQGD-----	YPKDVSLEERRKGAILHVIGMIYMFIALAIVCD	155
Qy	97	R-FMASIEVITSQEREVTIKKPNGETSTTTIRVWNETVSNLTLMALGSSAPEILLSLIEV	155	
		: : :	: : : : :	
Db	156	EFFVPSLTVITEK-----	LGI-SDDVAGATFMAAGGSAPELFTSLIGV	197
Qy	156	CGHGFIGA-GDLGPSTIVGSAAFNMFIIIGICVYVIPDGETR	KIKHLRVFFITAAWSIFAY	214
		: : : : :	: : : :	
Db	198	----FIAHSNVGIGTIVGSAFVNILFVIGMCALF-----	SREILNL-----TWWPLFRD	242
Qy	215	IWLY-----MILAVFSPGVVQVWEGLLTL-FFFPVCVLL-----	AWVADKRLLFYKYM	261
		: :: : : :		
Db	243	VSFYIVDLIMLIIFFLDNVIMWWESLLLLTAYFAYVVF	MKFNVQVERWV-----	291
Qy	262	HKKYRTDKHRGIII-----	ETEGD-----HPKGIEMDGK-----MMNS---	294
		: : : : :	: : :	
Db	292	--KQMINRNKVVKVTVSE	AQAKASTAGDKEEPTLPNKPRLQRGGSASLHNSLMRNSIFQ	349
Qy	295	---HFLDGNLVPLE-----	GK-----EVDESR-REMIRILKDLKQKHPEKDLDQ----	334
			: : : : :	
Db	350	LMIHTLD-----	PLAEELGSYGKLYYDTMTEEGRFREKASILHAKKCCQVDENERQNG	405
Qy	335	LVE MANYYALSHQQKSRAFYRIQATRM	MTGA-----GNILKKHAAEQAKKASSMSEVHTD	389
		: : : : : :	: : : :	
Db	406	AANHVDYAAEKIELPNSTSTEVE	MTSPSSEASEPVQNGNLSHSIEAADAPQATETAEDDD	465
Qy	390	EP	391	
		:		
Db	466	QP	467	

Search completed: June 24, 2004, 16:12:40
Job time : 12.6677 secs